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NON-A, NON-B HEPATITIS VIRUS GENOME, POLYNUCLEOTIDES,
POLYPEPTIDES, ANTIGEN, ANTIBODY AND DETECTION SYSTEMS. ;

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ABSTRACT:

Non-A, non-B hepatitis (NANB hepatitis) virus RNA and its corresponding polypeptide, related antigen, antibody, and detection systems for detecting NANB hepatitis antigen or antibodies.

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(54) **Non-A, Non-B Hepatitis virus genome, polynucleotides, polypeptides, antigen, antibody and detection systems.**

(57) **Non-A, non-B hepatitis (NANB hepatitis) virus RNA and its corresponding polypeptide, related antigen, antibody, and detection systems for detecting NANB hepatitis antigen or antibodies.**

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Reference To A Related Application

The present application is a continuation-in-part of our copending U.S. Patent Application Serial No. 07/866,045, filed on April 9, 1992, which is incorporated by reference in its entirety.

Background of the Invention

The present invention concerns non-A, non-B hepatitis (hereinafter called NANB hepatitis) virus genome, polynucleotides, polypeptides, related antigen, antibody and detection systems for detecting NANB antigens or antibodies.

Viral hepatitis of which DNA and RNA of the causative viruses have been elucidated, and their diagnosis and even prevention in some have been established, are hepatitis A and hepatitis B. The general name NANB hepatitis was given to the other forms of viral hepatitis.

Post-transfusion hepatitis was remarkably reduced after introduction of diagnostic systems for screening hepatitis B in transfusion bloods. However, there are still an estimated 280,000 annual cases of post-transfusion hepatitis caused by NANB hepatitis in Japan.

NANB hepatitis viruses were recently named C, D and E according to their types, and scientists started a world wide effort to conduct research for the causative viruses and subsequent extermination of the causative viruses.

In 1988, Chiron Corp. claimed that they had succeeded in cloning RNA virus genome, which they termed hepatitis C virus (hereinafter called HCV), as the causative agent of NANB hepatitis and reported on its nucleotide sequence (British Patent 2,212,511 which is the equivalent of European Patent Application 0,318,216). HCV (C100-3) antibody detection systems based on the sequence are now being introduced for screening of transfusion bloods and for diagnosis of patients in Japan and in many other countries. The detection systems for the C100-3 antibody have proven their partial association with NANB hepatitis; however, they capture only about 70% of carriers and chronic hepatitis patients, or they fail to detect the antibody in acute phase infection, thus leaving problems yet to be solved even after development of the C100-3 antibody by Chiron Corp.

The course of NANB hepatitis is troublesome and most patients are considered to become carriers, then to develop chronic hepatitis. In addition, most patients with chronic hepatitis develop liver cirrhosis, then hepatocellular carcinoma. It is therefore very imperative to isolate the virus itself and to develop effective diagnostic reagents enabling earlier diagnosis.

The presence of a number of NANB hepatitis which cannot be diagnosed by Chiron's C100-3 antibody detection kits suggests a possibility of a difference in subtype between Chiron's HCV and Japanese NANB hepatitis virus.

In order to develop NANB hepatitis diagnostic kits of more specificity and to develop effective vaccines, it becomes an absolutely important task to analyze each subtype of NANB hepatitis causative virus at its genetic and corresponding amino acid level.

Summary of the Invention

An object of the present invention is to provide the nucleotide sequence coding for the structural protein of NANB hepatitis virus and, with such information, to analyze amino acids of the protein to locate and provide polypeptides useful as antigen for establishment of detection systems for NANB virus, its related antigens and antibodies.

A further object of the present invention is to locate polynucleotides essential to treatment, prevention and diagnosis, and polypeptides effective as antigens, by isolating NANB hepatitis virus RNA from human and chimpanzee virus carriers, cloning the cDNA covering the whole structural gene of the virus to determine its nucleotide sequence, and studying the amino acid sequence of the cDNA. As a result, the inventors have determined the nucleotides of the whole genome of a strain of NANB virus called HC-J6 and a strain called HC-J8. NANB hepatitis virus genome of HC-J6 and HC-J8 differ from that of Chiron's HCV.

Brief Description of the Drawings

Figure 1 shows the restriction map and structure of the coding region of NANB hepatitis virus genome (HC-J6) and positions of clones. C, E, NS-1, NS-2, NS-3, NS-4 and NS-5 are the abbreviation of core, envelope, non-structure-1, -2, -3, -4 and -5.

Figures 2 to 4 show method of determination of the nucleotide sequence of 5' terminus of NANB hepatitis virus genome of strains HC-J1, HC-J4 and HC-J6 respectively.

Figure 5 shows the method of determination of the nucleotide sequence of 3' terminus of HC-J6 genome. Solid lines show nucleotide sequences determined by clones from libraries of bacteriophage lambda gt10, and broken lines show nucleotide sequences determined by clones obtained by PCR.

Figure 6 shows the structure of coding region of NANB hepatitis virus genome (HC-J8) and positions of clones. Regions a to n indicate positions of amplification by PCR.

Detailed Description of the Invention

The present invention provides NANB hepatitis virus genome RNA for strain HC-J6 (sequence list 1) consisting of 340 nucleotides on the 5' terminus that follow an open reading frame consisting of 9099 nucleotides coding for the structural protein and non-structural protein that follow a noncoding region consisting of 150 nucleotides containing an U-stretch consisting of 108 uracils on the 3' terminus of NANB hepatitis virus, and NANB hepatitis virus genome having substantially the nucleotide sequence of sequence list 1.

The present invention provides polynucleotide N-9589 (strain HC-J6) comprising the DNA nucleotide sequence of sequence list 2; cDNA clone J6-ø81 comprising the nucleotide sequence of sequence list 3; cDNA clone J6-ø8 comprising the nucleotide sequence of sequence list 4; and NANB hepatitis virus polynucleotides having substantially the sequence of nucleotides of NANB hepatitis virus nucleotides shown in sequence lists 2 through 4.

The invention provides polypeptide coded for by genome or polynucleotide of HC-J6 above, polypeptide P-J6-3033, comprising the polypeptide sequence of sequence list 5, polypeptides produced by using recombinant genome, recombinant polynucleotides and recombinant cDNA of whole or a part of cDNA above, and polyclonal or monoclonal antibodies against the polypeptides described above.

The present invention also provides NANB hepatitis virus genome for strain HC-J8 comprising sequence list 6, NANB hepatitis virus RNA consisting of noncoding region consisting of 341 nucleotides on 5' terminus followed by an open reading frame consisting of 9099 nucleotides coding for the structural protein and non-structural protein followed by a noncoding region consisting of 71 nucleotides containing an U-stretch consisting of 30 uracils on 3' terminus of NANB hepatitis virus comprising sequence list 6, and NANB hepatitis virus genome having substantially the nucleotide sequence of sequence list 6.

The present invention provides polynucleotide N-9511 for strain HC-J8 comprising the DNA nucleotide sequence of sequence list 7 and NANB hepatitis virus polynucleotide having substantially the sequence of nucleotides of NANB hepatitis virus nucleotides comprising sequence list 7.

The invention provides polypeptide coded for by genome or polynucleotide of HC-J8 above, polypeptide P-J8-3033, comprising the polypeptide sequence of sequence list 8 and polypeptide P-J8-3033-2 comprising the polypeptide sequence of sequence list 9, polypeptides produced by using recombinant genome, recombinant polynucleotides and recombinant cDNA of whole or a part of cDNA above, and polyclonal or monoclonal antibodies against the polypeptides described above.

The present invention, furthermore, provides NANB hepatitis diagnostic system using polypeptides or antibodies described above.

In the method described below, NANB hepatitis virus RNA of the present invention was obtained and its nucleotide sequence was determined.

Plasma samples (HC-J1, HC-J4, HC-J6 and HC-J8) were obtained from human and chimpanzee. HC-J1, HC-J6 and HC-J8 were obtained from Japanese blood donors who had tested positive for HCV antibody. HC-J4 was obtained from the chimpanzee subjected to the challenge test but was negative for Chiron's C100-3 antibody previously mentioned.

RNA was isolated from each of the plasma samples. Following the study of 5' terminus of approximately 2,500 nucleotides and 3' terminus of approximately 1,100 nucleotides disclosed in Japanese patent application No. 196175/91, the inventors have completed the study of the region coding for non-structural protein of strain HC-J6 and the study of the full length sequence of 9,589 nucleotides of HC-J6 genome RNA and have completed the study of the region coding for non-structural protein of strain HC-J8 and the study of the full length sequence of 9,589 nucleotides of HC-J8 genome RNA.

As described in the Example below, strain HC-J6 had a 5' noncoding region consisting of 340 nucleotides, and strain HC-J8 had a 5' noncoding region consisting of 341 nucleotides, followed by region coding for structural protein and region coding for non-structural protein.

Concerning the 3' terminus, strain HC-J6 was found to have a region consisting of 150 nucleotides containing an U-stretch consisting of 108 uracils following after the region coding for non-structural protein

and strain HC-J8 was found to have a region consisting of 71 nucleotides containing an U-stretch consisting of 30 uracils following after the region coding for non-structural protein.

The coding region starting with adenine (341st nucleotide from the 5' terminus for strain HC-J6 and 342nd nucleotide from the 5' terminus for strain HC-J8) was found to have a long *Open Reading Frame* consisting of 9099 nucleotides which codes for 3033 amino acids. HCV or hepatitis C virus is supposed to be closely allied to flavivirus in regard to its genetic structure. The coding of the NANB hepatitis virus genome of the present invention was considered to be consisting of regions named C (core), E (envelope), NS-1 (non-structural-1), NS-2 (non-structural-2), NS-3 (non-structural-3), NS-4 (non-structural-4) and NS-5 (non-structural-5).

As compared with the sequence of HCV disclosed in the European Patent Application by Chiron Corp. (Publication No. 388,232), homology of sequences of the strain HC-J6 was 67.9% for the full nucleotide sequence and 72.3% for the full amino acid sequence, and homology of sequences of the strain HC-J8 was 66.4% for the full nucleotide sequence and 71.0% for the full amino acid sequence.

From an examination of homology for regions, the homology of nucleotide sequences (strain HC-J6) of the 5' terminal noncoding region was 94.4% and that of the amino acid sequences of the C region was 90.1%, showing comparatively high homology; on the other hand, concerning lower stream than envelope, homologies of amino acid sequence were found to be as low as 60.4% for E, 71.1% for NS-1, 57.8% for NS-2, 81.1% for NS-3, 73.1% for NS-4, and 69.9% for NS-5. As a result, HC-J6 strain was found to be significantly different from HCV strain found by Chiron Corp.

From an examination of homology for regions, the homology of nucleotide sequences (strain HC-J8) of the 5' terminal noncoding region was 93.8% and that of the amino acid sequences of the C region was 90.1%, showing comparatively high homology; on the other hand, concerning lower stream than envelope, homologies of amino acid sequence were found to be as low as 54.7% for E, 73.1% for NS-1, 55.6% for NS-2, 81.3% for NS-3, 72.1% for NS-4, 67.3% for NS-5, and 25.9% for 3' terminal noncoding region. As a result, HC-J8 strain was found to be significantly different from HCV strain found by Chiron Corp.

From the comparison of amino acid sequence of HC-J6 strain with strain HC-J1 (American type) and strain HC-J4 (Japanese type) disclosed by the inventors (Japan. J. Exp. Med. (1990), 60: 167-177), homology in the core region was more than 90% for each strain while that in the envelope region was 60.9% for HC-J1 and 53.1% for HC-J4. Thus, in the present invention, strain HC-J6 was found to be a different type of virus than strains HC-J1 or HC-J4.

From the comparison of amino acid sequence of HC-J8 strain with strain HC-J1 (type I) and strain HC-J4 (type II), homology of approximately 3,000 nucleotides of 5' terminus was 70.1% for HC-J1 and 67.1% for HC-J4, and from the comparison of all nucleotides with HC-J6 (type III) genome homology was as low as 76.9%. On the other hand, HC-J8 showed high homology with strain HC-J7 (type IV) disclosed in Japanese patent application 196175/91 as 93.1% for approximately 3,000 nucleotides of 5' terminus.

Nucleotides among strains assumed to belong to same type were supposed to show high homology. For example, homology of 95.6% for approximately 3,000 nucleotides of 5' terminus between HCV disclosed by Chiron Corp. and HC-J1 appears to show that they should be classified into type I. On the other hand, low homology of HC-J8 with HCV, HC-J1, HC-J4 and HC-J6 appeared to show that it was not to be classified into type I, II or III, but into type IV (the same as HC-J7).

Strain HC-J8 has some mutations in the nucleotides as shown in sequence lists 6 and 7 by symbols M, R, W, S, Y, K and B. It also can be easily understood that it has some mutations of amino acids from comparison of sequences in sequence lists 8 and 9. Mutation of nucleotides was observed up to approximately 1.4% in the whole genome and that of amino acids was observed up to approximately 1.7% in whole ORF. Thus the present invention includes genomes, polynucleotides and polypeptides of strain HC-J8 having some mutations.

In addition, envelope (E) region (576 nucleotides/192 amino acids of amino acids 192-383) and NS-1 region (1050 nucleotides/350 amino acids of amino acids 384-733) having many mutations in HC-J8 are called hyper-variable region since mutations were observed as 20 nucleotides/7 amino acids (3.47%/3.64%) in E region and 37 nucleotides/19 amino acids (3.52%/5.42%) in NS-1 region. According to these findings, the present invention can be recognized to include genomes and polypeptides coded for by the genomes of strain HC-J8 having mutations of 3.5% to 5.5% in those regions.

The genome, polynucleotide, and cDNA clones of the present invention can be used as material to produce peptides of the invention by integration into a host genome, e.g. *E. coli* or *Bacillus*, by means of known genetic engineering techniques.

Polypeptides of the invention are useful as material for diagnostic agents to detect NANB hepatitis antibodies with high specificity and as material to produce polyclonal and monoclonal antibodies by known techniques.

Polyclonal and monoclonal antibodies of the invention are useful as materials for diagnostic agents to detect NANB hepatitis antigens with high specificity.

A detection system using each polypeptide of the present invention or polypeptide with partial replacement of amino acids, and a detection system using monoclonal or polyclonal antibodies to such polypeptides, are useful as diagnostic agents of NANB hepatitis with high specificity and are effective to screen out NANB hepatitis virus from transfusion bloods or blood derivatives. The polypeptides, or antibodies to such polypeptides, can be used as a material for a vaccine against NANB hepatitis virus.

It is well known in the art that one or more nucleotides in a DNA sequence can be replaced by other nucleotides in order to produce the same protein. The present invention also concerns such nucleotide substitutions which yield DNA sequences which code for polypeptides as described above. It is also well known in the art that one or more amino acids in an amino acid sequence can be replaced by equivalent other amino acids, as demonstrated by U.S. Patent No. 4,737,487 which is incorporated by reference, in order to produce an analog of the amino acid sequence. Any analogs of the polypeptides of the present invention involving amino acid deletions, amino acid replacements, such as replacements by other amino acids, or by isosteres (modified amino acids that bear close structural and spatial similarity to protein amino acids), amino acid additions, or isosteres additions can be utilized, so long as the sequences elicit antibodies recognizing NANB antigens.

Examples of application of this invention are shown below, however, the invention shall in no way be limited to those examples.

Examples

The 5' terminal nucleotide sequence and amino acid sequence of NANB hepatitis virus genome were determined in the following way:

(1) Isolation of RNA

RNA of the sample (HC-J1, HC-J6, HC-J8) from plasma of Japanese blood donor testing positive for HCV (C100-3) antibody (by Ortho HCV Ab ELISA, Ortho Diagnostic System, Tokyo), and that of the sample (HC-J4) from the chimpanzee challenged with NANB hepatitis for infectivity and negative for HCV antibody were isolated in the following method:

Each plasma sample was added with Tris chloride buffer (10 mM, pH 8.0) and centrifuged at 68×10^3 rpm for 1 hour. Its precipitate was suspended in Tris chloride buffer (50 mM, pH 8.0) containing 200 mM NaCl, 10 mM EDTA, 2% (w/v) sodium dodecyl sulfate (SDS), and proteinase K 1 mg/ml, incubated at 60 °C for 1 hour, then their nucleic acids were extracted by phenol/chloroform and precipitated by ethanol to obtain RNA.

(2) HC-J1 and HC-J8 cDNA Synthesis

After heating the RNA isolated from HC-J1 or HC-J8 plasma at 70 °C for 1 minute, this was used as a template; 10 units of reverse transcriptase (cDNA Synthesis System Plus, Amersham Japan) and 20 pmol of oligonucleotide primer (20 mer) were added and incubated at 42 °C for 1.5 hours to obtain cDNA. Primer #8 (5'- GATGCTTGCGGAAGCAATCA - 3') was prepared by referring to the basic sequence shown in European Patent Application No. 88310922.5, which is relied on and incorporated herein by reference.

(3) cDNA Was Amplified by the following Polymerase Chain Reaction (PCR)

cDNA was amplified for 35 cycles according to Saiki's method (Science (1988) 239: 487-491) using Gene Amp DNA Amplifier Reagent (Perkin-Elmer.Cetus) on a DNA Thermal Cycler (Perkin-Elmer.Cetus).

For cDNA synthesis and for PCR for HC-J8, synthesized primers disclosed in Japanese patent application 153402/90 and those based on HC-J1, HC-J4 and HC-J6 genomes disclosed in Japanese patent applications 196175/91 and b low were utilized.

(4) Determination of 5' Terminal Nucleotide Sequence of HC-J1 and HC-J4 by Assembling cDNA Clones

As shown in Figures 2 and 3, nucleotide sequences of 5' termini of the genomes of strains HC-J1 and HC-J4 were determined by combined analysis of clones obtained from the cDNA library constructed in bacteriophage λ gt10 and clones obtained by amplification of HCV specific cDNA by PCR.

Figures 2 and 3 show 5' termini of NANB hepatitis virus genome together with cleavage site by restriction endonuclease and sequence of primers used. In the figures, solid lines are nucleotide sequences determined by clones from bacteriophage λ gt10 library while dotted lines show sequences determined by clones obtained by PCR.

A 1656 nucleotide sequence of HC-J1 spanning nt454-2109 was determined by clone ϕ 41 which was obtained by inserting the cDNA synthesized with the primer #8 into λ gt10 phage vector (Amersham).

Another primer #25 (5'-TCCCTGTTGCATAGTTCACG-3') corresponding to nt824-843 was synthesized based on the ϕ 41 sequence, and four clones (ϕ 60, ϕ 61, ϕ 66 and ϕ 75) were obtained to cover the upstream sequence nt18-843.

(5) Determination of 5' Terminal Nucleotide Sequence of HC-J6.

The nucleotide sequence of the 5' terminus of strain HC-J6 was determined from analysis of clones obtained by PCR amplification as shown in Figure 4.

Isolation of RNA from HC-J6 and determination of its sequence was made in the same manner as described in (2) above. Sequences in the range of nt24-2551 of the RNA were determined from consensus sequence of respective clones obtained by amplification by PCR using each pair of primers based on nucleotide sequence of HC-J4.

nt24-826

#32 (5'-ACTCCACCATAGATCACTCC-3')

#122 (5'-AGGTTCCTGTTGCATAATT-3')

Clones: C9397, C9388, C9764

nt732-1907

#50 (5'-GCCGACCTCATGGGGTACAT-3')

#128 (5'-TCGGTCGTGCCCCACTACCAC-3')

Clones: C9316, C9752, C9753

nt1847-2571

#149 (5'-TCTGTGTGTGGCCCAGTGTA-3')

#146 (5'-AGTAGCATCATCCACAAGCA-3')

Clones: C11621, C11624, C11655

In order to determine further upstream of the 5' terminus, antisense primer #36 (5'-AACACTACTCGGCTAGCAGT-3') corresponding to nt246-265, followed by dAs were added to 5' terminus of cDNA using terminal deoxynucleotidyl transferase, and one-sided PCR amplification was made twice as described below.

cDNA was amplified for 35 cycles as first stage PCR using oligo dT primer (20-mer) and antisense primer #48 (5'-GTTGATCCAAGAAAGGACCC-3') of nt188-207, followed by the second stage of PCR by 30 cycle amplification using the first PCR product as a template, oligo dT primer (20-mer) and antisense

primer #109 (21-mer; 5'-ACCGGATCCGACAGACCACTAT-3') corresponding to nt140 to 160. The obtained PCR product was subcloned to M13 phage vector.

Nucleotide sequence from nt1 to 23 was determined from consensus sequence of 13 isolated clones C9577, C9579, C9581, C9587, C9590, C9591, C9595, C9606, C9609, C9615, C9616 and C9619 obtained above which were considered having complete 5' terminus.

(6) Determination of nucleotide sequence of HC-J6 middle region.

cDNA library was constructed with using λ gt10 according to the method described in (2) above from 100ml of HC-J6 plasma as a starting materials. Primers #162 and #81 were prepared for synthesis by referring to the basic sequence shown in the European Patent Application Publication No. 318,216. Clones were selected by plaque hybridization.

Nucleotide sequence from 2552 to 8700 was determined from consensus sequence of four obtained cDNA clones ϕ 2 (nt6996 to 8700), ϕ 6(nt6485 to 8700), ϕ 8(nt6008 to 8700) and ϕ 81 (nt2199 to 6168) as shown in Figure 1. Clones ϕ 81 and ϕ 8 were found to have nucleotide sequences shown in sequence lists 3 and 4 respectively.

(7) Determination of 3' terminal nucleotide sequence of HC-J6 strain.

As shown in Figure 5, the nucleotide sequence of the 3' terminus of HC-J6 genome was determined by analysis of clones obtained by amplification of HCV specific cDNA by PCR.

Nucleotide sequence of HC-J6 from nt8701 to 9241 was determined from consensus sequence of three clones consisting of 938 nucleotides, C9760, C9234 and C9761, obtained by amplification of sample using primer #80 (5'-GACACCCGCTGTTTGGACTC-3') and #60 (5'-GTTCTTACTGCCAGTTGAA-3').

Nucleotide sequence of 3' terminus downstream from nt9242 was determined in the method described below.

Isolation of RNA from HC-J6 was made in the same manner as described in (1) above. The obtained RNA was added poly (A) to its 3' terminus using poly (A) polymerase and cDNA was synthesized using oligo (dT)₂₀ as a primer, and obtained cDNA was provided to PCR as a template.

First PCR product was made with using #97 (5'-AGTCAGGGCGTCCCTCATCT-3') as a sense primer and oligo (dT)₂₀ as an antisense primer. Second PCR product was made with using #90 (5'-GCCGTTTGCGGCCGATATCT-3') corresponding to downstream sequence of #97 as a sense primer, and oligo (dT)₂₀ as an antisense primer as well as first PCR product. PCR product obtained by two step amplification was smoothened on both ends by treatment with T₄ DNA polymerase, followed by phosphorylation of 5' terminus by T₄ polynucleotide kinase. The obtained product was subcloned into Hinc II position of M13mp19 phage vector.

Nucleotide sequence of 3' terminus was determined from consensus sequence of 19 obtained clones, C10311, C10313, C10314, C10320, C10322, C10323, C10326, C10328, C10330, C10333, C10334, C10336, C10337, C10345, C10346, C10347, C10349, C10350 and C10357.

As a result, the nucleotide sequence of cDNA to HC-J6 genome RNA was determined as shown in sequence list 2, and full sequence of genome RNA was determined as shown in sequence list 1.

(8) Determination of amino acid sequences.

According to the nucleotide sequence of the genome of strain HC-J6, determination was made of sequence of coded region starting with ATG. As a result, HC-J6 genome was found to have a long *Open Reading Frame* coding for polypeptide precursor consisting of 3033 amino acid residues.

(9) Determination of 5' terminal nucleotide sequence of HC-J8

As shown in Figure 6, the nucleotide sequence of 5' terminus of HC-J8 genome (a region) was determined by analysis of clones obtained by amplification of HCV specific cDNA by PCR.

Single-stranded cDNA was synthesized using antisense primer #36 (5'-AACACTACTCGGCTAGCAGT-3') of nt246 to 265 in the same manner as (2) above, then it was added with dATP tail at its 3' terminus by terminal deoxynucleotidyl transferase, then amplified by one-sided PCR in two stages.

That is, in the first stage, antisense primer #48 (5'-GTTGATCCAAGAAAGGACCC-3') of nt188 to 207 was used with sense primer selected from non-specific primer #165 (5'-AAGGATCCGTCGACATCGATAAT-ACG (A)₁₇-3') and #171 (5'-AAGGATCCGTCGACATCGATAATACG(T)₁₇-3') to amplify the dA-tailed cDNA

by PCR for 35 cycles; and in the second stage, using the product of the first-stage PCR as a template, non-specific primer #166 (5' AAGGATCCGTCGACATCGAT -3') and antisense primer #109 (21-mer; 5'-ACCGGATCCGCAGACCACTAT -3') were added to initiate PCR for 30 cycles. The product of PCR was subcloned to M13 phage vector.

5 Thirteen independent clones (poly dT-tailed: C14951, C14952, C14953, C14958, C14960, C14968, C14971, C14972 and C14974; poly dA-tailed: C14987, C14996, C14999 and C15000) were obtained (each considered having complete length of 5' terminus), and the consensus sequence of nt1-139 of the respective clones was determined.

10 (10) cDNA amplification of ORF region and 3' terminus by PCR

As shown in Figure 6, the nucleotide sequence of downstream from nt140 of HC-J8 genome was determined by analysis of clones obtained by amplification of HCV specific cDNA by PCR.

15 Single-stranded cDNAs to HC-J8 RNA were synthesized in the same manner as (2) above using antisense primers described below, then they were amplified by PCR using sense and antisense primers described below. Each product of PCR was subcloned to M13 phage vector, then consensus sequence of the respective clones of each region was determined.

The primers for cDNA synthesis and PCR amplification, and the numbers of obtained clones are shown below for each region. Alphabetical symbol of each amplified region corresponds to that in Figure 6.

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b region

nt45-847

5 Primer for cDNA synthesis: #122 (5'-AGGTTCCCTGTTGCATAATT-3')

Primer for PCR: sense: #32A (5'-CTGTGAGGAACTACTGTCTT-3')

10 antisense #122

Clones: C15221,C15222,C15223

15 c region

nt732-1354

20 Primmer for cDNA synthesis:#54 (5'-ATCGCGTACGCCAGGATCAT-3')

Primer for PCR: sense: #50 (5'-GCCGATCTCATGGGGTACAT-3')

antisense:#54

25 Clones: C15256,C15257,C15258

30 d region

ntl300-1879

Primer for cDNA synthesis: #199 (5'-GGGGTGAAACAATACACCGG-3')

35 Primer for PCR: sense: #205 (5'-GGGACATGATGATCAACTGG-3')

antisense: #199

40 Clones: C14221,C14222,C14223

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e region

ntl833-2518

5 Primer for cDNA synthesis: #146 (5'-AGTAGCATCATCCACAAGCA-3')
 Primer for PCR: sense: #150 (5'-ATCGTCTCGGCTAAGACGGT-3')
 10 antisense: #146
 Clones: C11535,C11540,C11566

15 f region

nt2433-3451

20 Primer for cDNA synthesis: #170 (5'-GCATAAGCAGTGATGGGGGC-3')
 Primer for PCR: sense: #160 (5'-CAGAACATCGTGGACGTGCA-3')
 antisense: #170
 25 Clones: C15348,C15349,C15356

30 g region

nt3404-4300

Primer for cDNA synthesis: #225 (5'-TCGCATATGATGATGTCATA-3')
 35 Primer for PCR: sense: #238 (5'-CTACACCTCCAAGGGGTGGA-3')
 antisense: #225
 40 Clones: C15701,C15702,C15703

h region

45 nt4221-5015

Primer for cDNA synthesis: #216 (5'-GTGGTCTAGACATACGGGCA-3')
 50 Primer for PCR: sense: #230 (5'-CCCATCACGTACTCCACATA-3')
 antisense: #216

55

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Clones: C15391,C15392,C15393

5 i region

nt4695-5062

Primer for cDNA synthesis: #210 (5'-GCATCTATGTGTGTGAGGCC-3')

10 Primer for PCR: sense: #209 (5'-TTCGACTCCGTGATCGACTG-3')

antisense: #210

15 Clones: C14087,C14088,C14089

j region

20 nt5021-6169

Primer for cDNA synthesis: #162 (5'-TCCGACTCCGTCACGTAGTG-3')

25 Primer for PCR: sense: #227 (5'-GTTCTGGGAAGCGGTCTTTA-3')

antisense: #162

Clones: C15421,C15422,C15423

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k region

35 nt6027-6889

Primer for cDNA synthesis: #232 (5'-GATGGGTCTGTTAGCATGGA-3')

Primer for PCR: sense: #242 (5'-TTGGTAGTGGGAGTCATCTG-3')

40 antisense: #232

Clones: C15733,C15734,C15735

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l region

nt6834-7735

50 Primer for cDNA synthesis #239 (5'-ATCGGTAACCTCTCCTCTTC-3')

55

Primer for PCR: sense: #241 (5'-CCTTGCGATCCTGAACCTGA-3')
antisense: #239

Clones: C15798, C15799, C15800

n region

nt7656-8630

Primer for cDNA synthesis: #222 (5'-GACCAGGTCGTCTCCACACA-3')

Primer for PCR: sense: #229 (5'-GTCGTGTGCTGCTCCATGTC-3')
antisense: #222

Clones: C15376, C15378, C15381

n region

nt8325-9511

Primer for cDNA synthesis: #165

Primer for PCR: sense: #80 (5'-GACACCCGCTGTTTTGACTC-3')
non-specific: #165

Clones: C15270, C15271, C15272

From the analysis described above, full nucleotide sequence of cDNA to HC-J8 was determined as shown in sequence list 7, then full nucleotide sequence of HC-J8 genome RNA as shown in sequence list 6. Two amino acid sequences shown in sequence lists 8 and 9 represent those coded for by HC-J8 genome.

Utilizing known immunological techniques, it is possible to determine epitopes (e.g., from the core region, etc.) from the polypeptides of sequence lists 5, 8 and 9. Determination of such epitopes of the NANB hepatitis virus opens access to chemical synthesis of the peptide, manufacturing of the peptide by genetic engineering techniques, synthesis of the polynucleotides, manufacturing of the antibody, manufacturing of NANB hepatitis diagnostic reagents, and development of products such as NANB hepatitis vaccines.

According to the well-known method described by Merrifield, NANB peptides can be synthesized. Furthermore, the polynucleotides in sequence lists 2-4 and 7 can be used to express polypeptides in host cells such as *Escherichia coli* by means of genetic engineering technique.

A detection system for antibody against NANB hepatitis virus can be developed using polyvinyl microtiter plates and the sandwich method. For example, 50 μ l of 5 μ g/ml concentration of a NANB peptide can be dispensed in each well of the microtiter plates and incubated overnight at room temperature for consolidation. The microplate wells can be washed five times with physiological saline containing 0.05% Tween 20. For overcoating, 100 μ l of NaCl buffer containing 30% (v/v) of calf serum and 0.05% Tween 20 (CS buffer) can be dispensed in each well and discarded after incubation for 30 minutes at room temperature.

For determination of NANB antibodies in samples, in the primary reaction, 50 μ l of the CS buffer containing 30% calf serum and 10 μ l of a sample can be dispensed in each microplate well and incubated on a microplate vibrator for one hour at room temperature. After completion of the reaction, microplate wells

can be washed five times in the same way as previously described.

In the secondary reaction, as labeled antibody 1 ng of horseradish peroxidase labeled anti-human IgG mouse monoclonal antibodies (Fab' fragment: 22G, Institut of Immunology Co., Ltd., Tokyo, Japan) dissolved in 50 µl of calf serum can be dispensed in each microplate well, and incubated on a microplate
 5 vibrator for one hour at room temperature. Wells can be washed five times in the same way. After addition of hydrogen peroxide (as substrate) and 50 µl of O-phenyldiamine solution (as color developer) in each well, and after incubation for 30 minutes at room temperature, 50 µl of 4M sulphuric acid can be dispensed in each well to stop further color development and for reading absorbance at 492 nm.

The cut-off level of this assay system can be set by measuring a number of donor samples with normal
 10 serum ALT (alanine aminotransferase) value of 34 Karmen unit or below and which tested negative for anti-HCV.

The present invention makes possible detection of NANB hepatitis virus infection which could not be detected by conventional determination methods, and provide NANB hepatitis detection kits capable of highly specific and sensitive detection at an early phase of infection.

15 These features allow accurate diagnosis of patients at an early stage of the disease and also help to remove at higher rate NANB hepatitis virus carrier bloods through screening test of donor bloods.

Polypeptides and their antibodies under this invention can be utilized for manufacture of vaccines and immunological pharmaceuticals, and structural gene of NANB hepatitis virus provides indispensable tools for detection of polypeptide antigens and antibodies.

20 Antigen-antibody complexes can be detected by methods known in this art. Specific monoclonal and polyclonal antibodies can be obtained by immunizing such animals as mice, guinea pigs, rabbits, goats and horses with NANB peptides (e.g., bearing NANB hepatitis antigenic epitope).

The present invention is based on studies on isolated virus genome of NANB hepatitis virus named HC-J6 and HC-J8, and is completed by clarification of the full sequence of the nucleotides. The invention
 25 makes possible highly specific detection of NANB hepatitis virus and provision of polypeptide, polyclonal antibody and monoclonal antibody to prepare the test system.

Further variations and modifications of the invention will become apparent to those skilled in the art from the foregoing and are intended to be encompassed by the claims appended hereto.

Japanese Priority Applications 287402/91 filed August 9, 1991 and 360441/91 filed on December 5,
 30 1991 are relied on and incorporated by reference. U.S. patent applications serial no. 07/540,604 (filed June 19, 1990), 07/653,090 (filed February 8, 1991), and 07/712,875 (filed June 11, 1991) are incorporated by reference in their entirety.

Sequence list

- 35
- Sequence list 1: whole nucleotides of HC-J6 genome RNA
 - Sequence list 2: N-9589 whole nucleotides of cDNA to HC-J6 genome RNA
 - Sequence list 3: J6-ø81 nucleotides of clone J6-ø81
 - Sequence list 4: J6-ø8 nucleotides of clone J6-ø8
 - 40 Sequence list 5: P-J6-3033 whole amino acids of ORF of HC-J6 genome
 - Sequence list 6: whole nucleotides of HC-J8 genome RNA
 - Sequence list 7: whole nucleotides of cDNA to HC-J8 genome RNA
 - Sequence list 8: whole amino acids of a variation of ORF of HC-J8 genome
 - Sequence list 9: whole amino acids of a variation of ORF of HC-J8 genome
- 45

Claims

1. Recombinant RNA of non-A, non-B hepatitis virus, strain HC-J6, comprising the nucleotide sequence of sequence list 1.
- 50 2. Recombinant cDNA of non-A, non-B hepatitis virus, strain HC-J6, comprising the nucleotide sequence of sequence list 2.
3. cDNA clone J6-ø81 comprising the nucleotide sequence of sequence list 3.
- 55 4. cDNA clone J6-ø8 comprising the nucleotide sequence of sequence list 4.

5. Amino acid sequence corresponding to recombinant cDNA of non-A, non-B hepatitis virus, strain HC-J6, comprising the amino acid sequence of sequence list 5.
6. Recombinant RNA of non-A, non-B hepatitis virus, strain HC-J8, comprising the nucleotide sequence of sequence list 6.
7. Recombinant cDNA of non-A, non-B hepatitis virus, strain HC-J8, comprising the nucleotide sequence of sequence list 7.
8. Amino acid sequence corresponding to recombinant cDNA of non-A, non-B hepatitis virus, strain HC-J8, comprising the amino acid sequence of sequence list 8.
9. Amino acid sequence corresponding to recombinant cDNA of non-A, non-B hepatitis virus, strain HC-J8, comprising the amino acid sequence of sequence list 9.
10. A non-A, non-B hepatitis diagnostic test kit for analyzing samples for the presence of antibodies directed against a non-A, non-B hepatitis antigen, comprising an antigen attached to a solid substrate and labeled anti-human immunoglobulin; wherein said antigen is an antigen selected from the antigens contained in sequence lists 5, 8 or 9.
11. A method of detecting antibodies directed against a non-A, non-B hepatitis antigen in a sample, said method comprising:
 - (a) reacting said sample with an antigen selected from the antigens contained in sequence lists 5, 8 or 9 to form antigen-antibody complexes; and
 - (b) detecting said antigen-antibody complexes.
12. A non-A, non-B hepatitis specific monoclonal or polyclonal antibody reactive with an antigen, said antigen is an antigen selected from the antigens contained in sequence lists 5, 8 or 9.
13. A method of detecting non-A, non-B hepatitis antigen in a sample, said method comprising:
 - (a) reacting said sample with the non-A, non-B hepatitis monoclonal or polyclonal antibody according to claim 12 to form antigen-antibody complexes; and
 - (b) detecting said antigen-antibody complexes.

Fig. 1

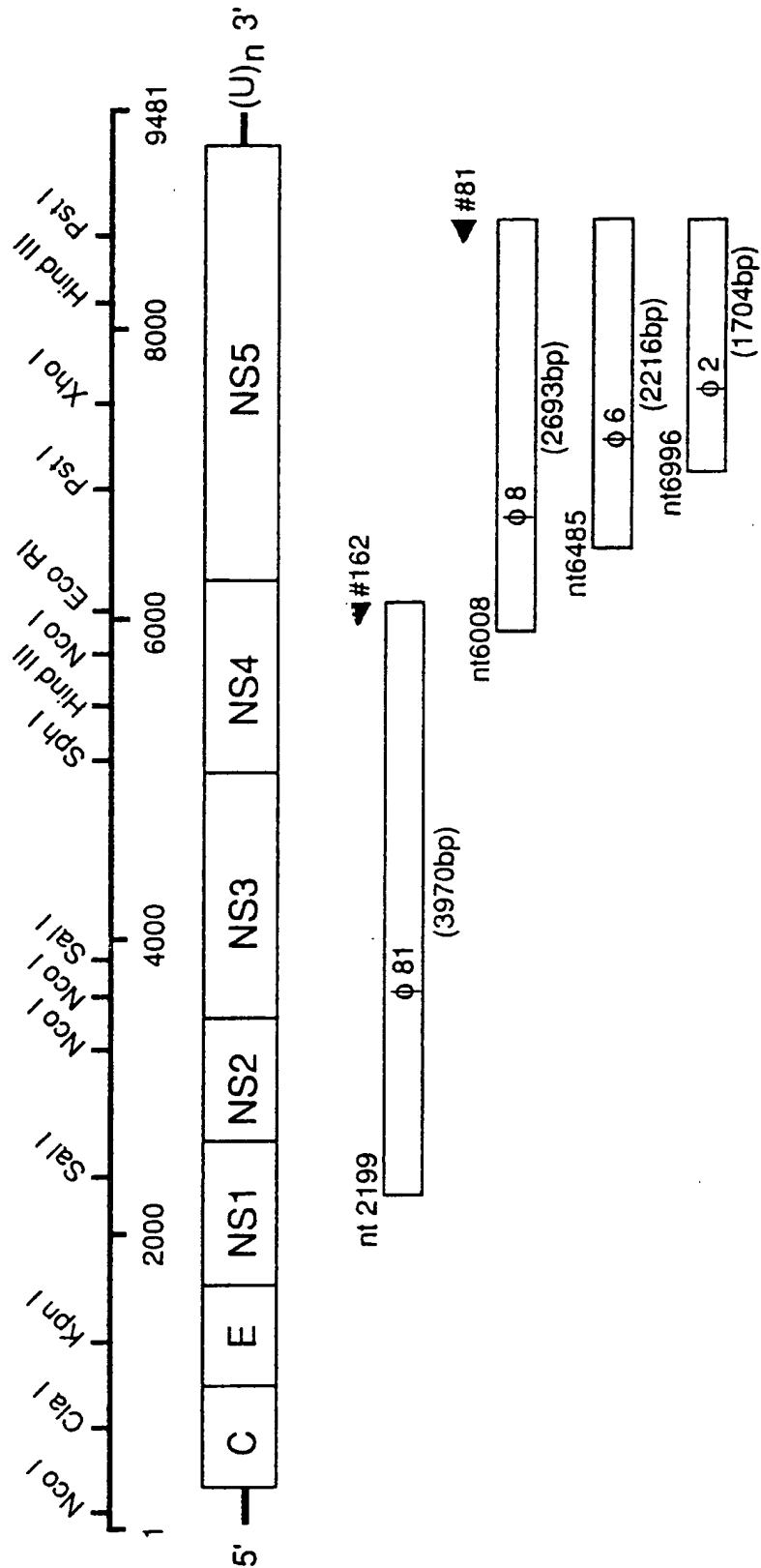


Fig. 2

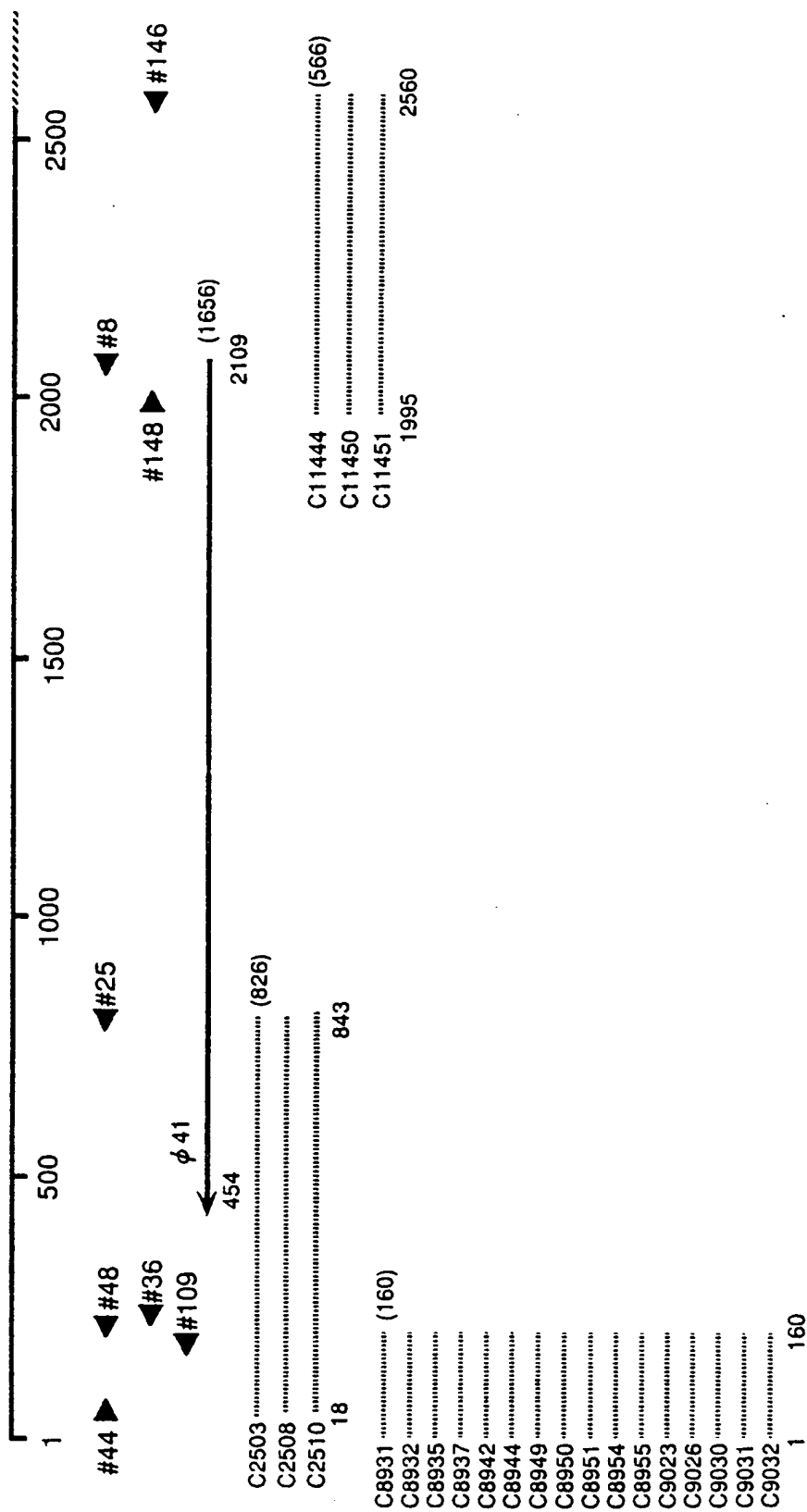


Fig. 3

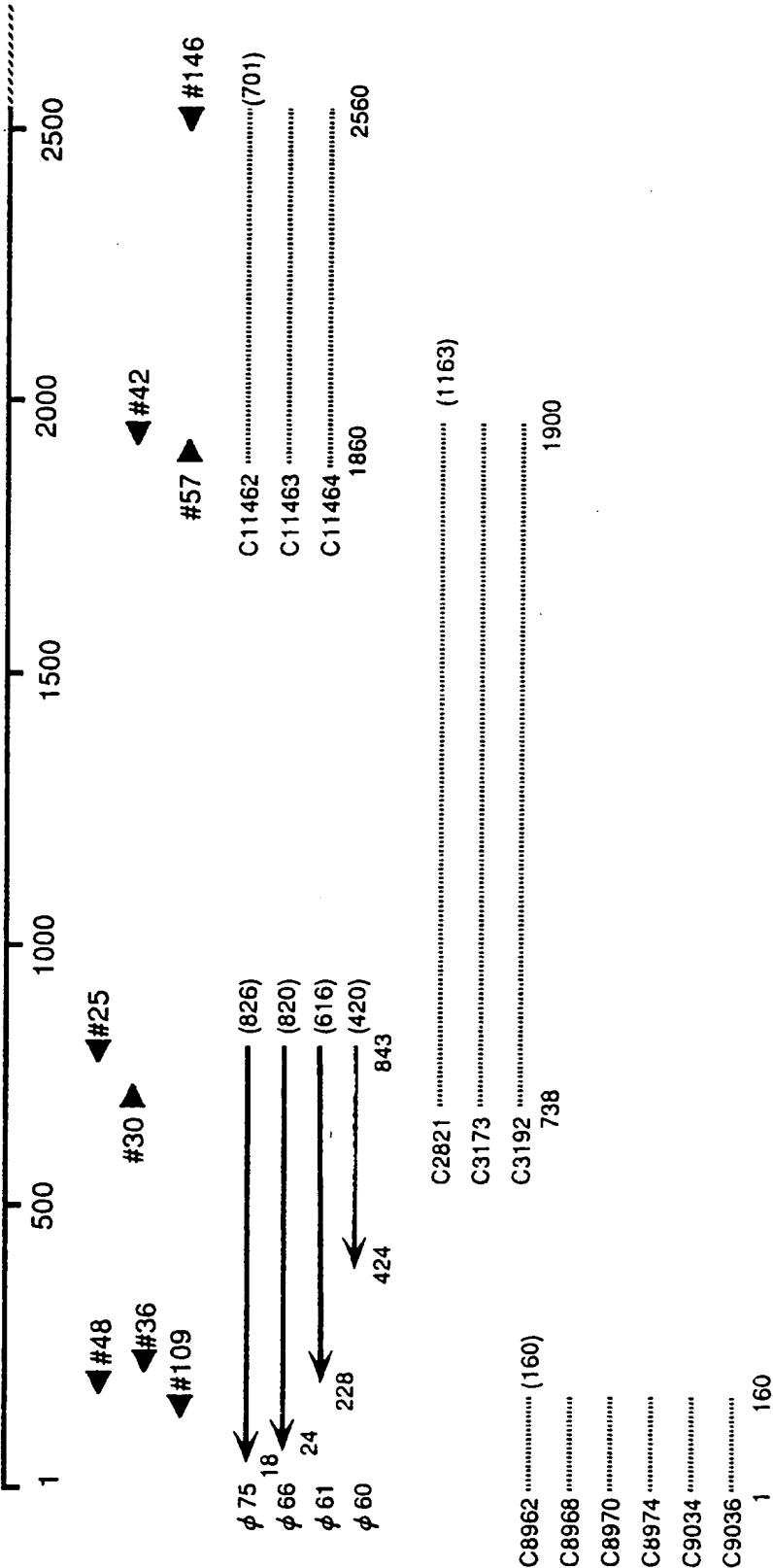


Fig. 4

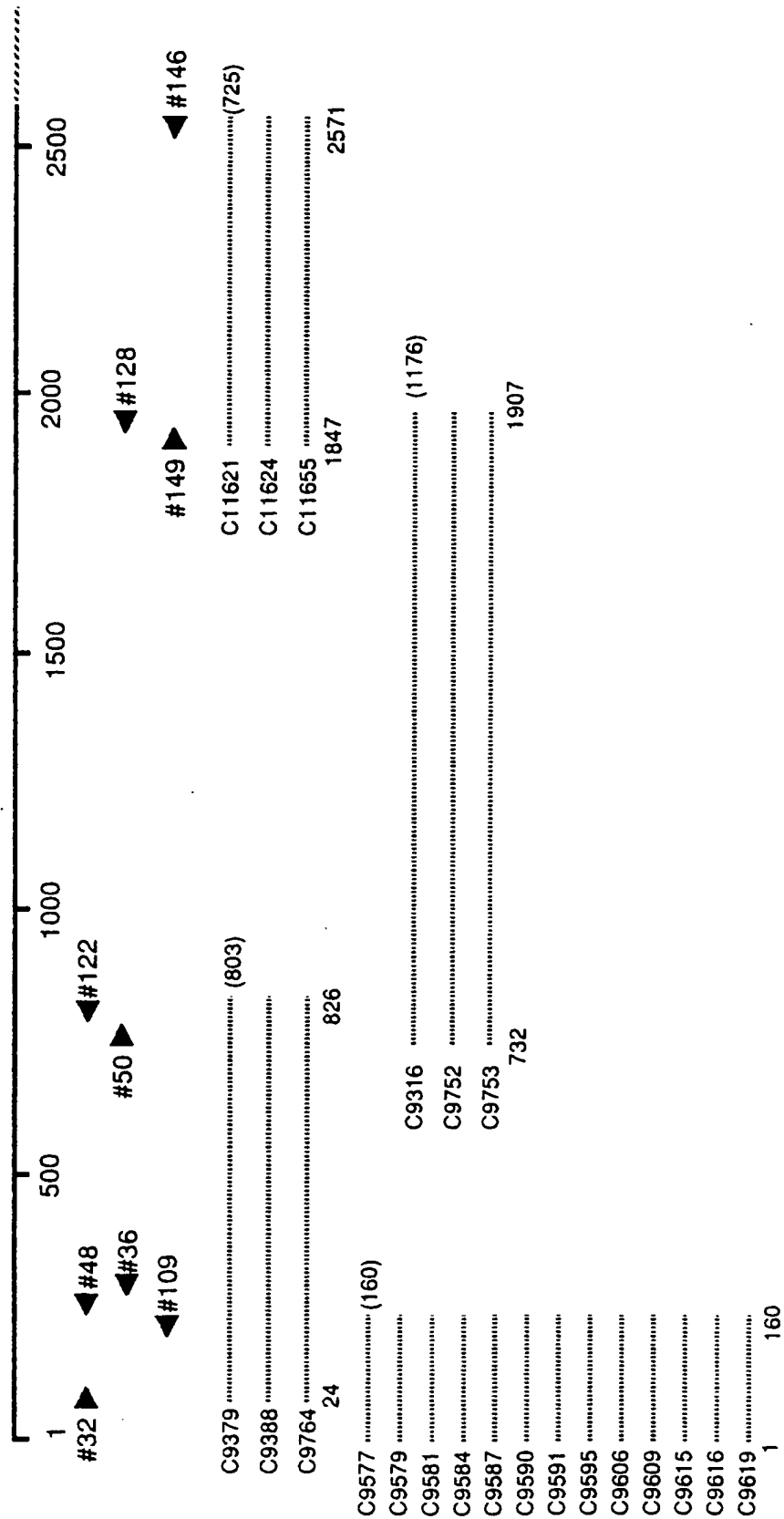


Fig. 5

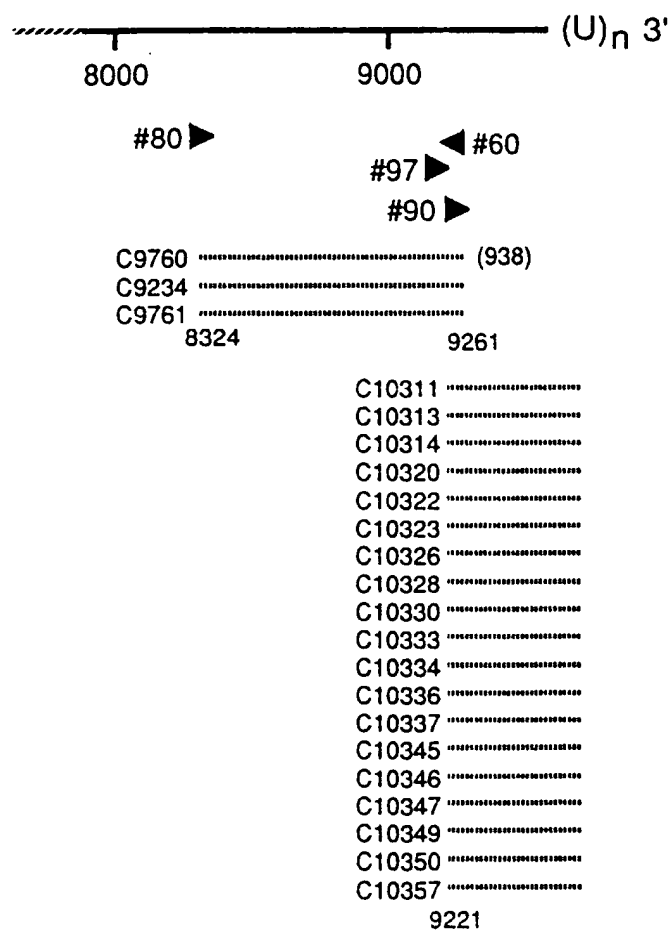
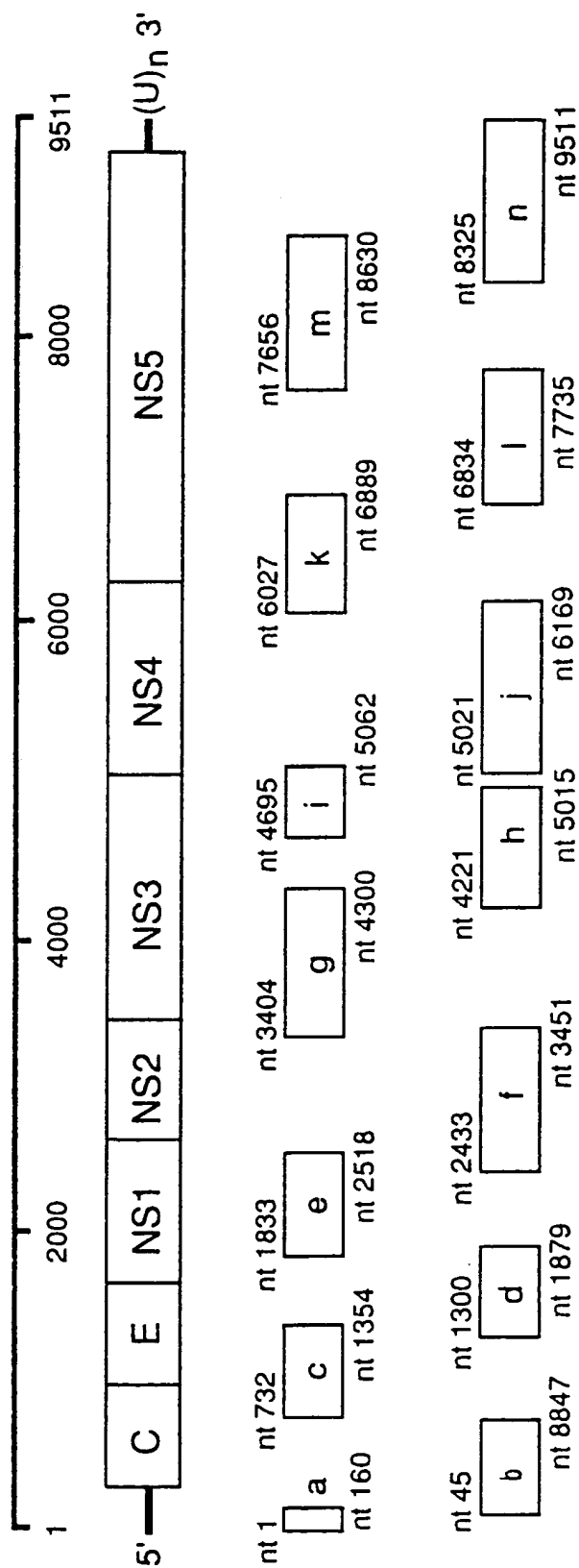


Fig. 6



Sequence ID No.1

Sequence Length: 9,589

Sequence Type: nucleic acid

Strandedness: single

Topology: linear

Molecule Type: genomic RNA

Method for Determination of Feature: E

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Sequence ID No.2
 Sequence Length: 9,589
 Sequence Type: nucleic acid
 Strandedness: single
 Topology: linear
 Molecule Type: cDNA to genomic RNA
 Method for Determination of Feature: E

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Sequence ID No.3
 Sequence Length: 3,970
 Sequence Type: nucleic acid
 Strandedness: single
 Topology: linear
 Molecule Type: cDNA to genomic RNA
 Method for Determination of Feature: E

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Sequence ID No.4
Sequence Length: 2,693
Sequence Type: nucleic acid
Strandedness: single
Topology: linear
Molecule Type: cDNA to genomic RNA
Method for Determination of Feature: E

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ACCATCCTAA CAGACTTTAA AAAGTGGCTG ACCTCCAAAT TGTTCCCAA GATGCCTGGT  360
CTCCCCTTTA TCTCTTGTCA AAAGGGGTAC AAGGGCGTGT GGGCTGGCAC TGGTATCATG  420
ACCACACGGT GTCCTTGCGG CGCCAATATC TCTGGCAATG TCCGCCTGGG CTCCATGAGA  480
ATTACGGGGC CCAAACCTG CATGAATATC TGGCAGGGGA CCTTTCCCAT CAATTGTTAC  540
ACGGAGGGCC AGTGCGTGCC GAAACCCGCA CCAAACCTTA AGATCGCCAT CTGGAGGGTG  600
GCGGCCTCAG AGTACGCGGA GGTGACGCAG CACGGGTCAT ACCACTACAT AACAGGACTT  660
ACCACTGATA ACTTGAAAGT TCCTTGCCAA CTACCTTCTC CAGAGTTCTT TTCCTGGGTG  720
GACGGAGTGC AGATCCATAG GTTTGCCCCC ATACCGAAGC CGTTTTTTCG GGATGAGGTC  780
TCGTTCTGCG TTGGGCTTAA TTCATTTGTC GTCGGGTCTC AGCTCCCTTG CGATCCTGAA  840
CCTGACACAG ACGTATTGAC GTCCATGCTA ACAGACCCAT CCCATATCAC GGCGGAGACT  900
GCAGCGCGGC GTTTGGCACG GGGGTCACCC CCGTCCGAGG CAAGCTCCTC AGCGAGCCAG  960
CTATCGGCAC CATCGCTGCG AGCCACCTGC ACCACCCACG GCAAGGCCTA TGATGTGGAC 1020
ATGGTGGATG CCAACCTGTT CATGGGGGCG GATGTGACCC GGATAGAGTC TGAGTCCAAA 1080
GTGGTCGTTT TGGACTCTCT CGACCCAATG GTCGAAGAAA GGAGCGACCT TGAGCCTTCG 1140
ATACCATCGG AATATATGCT CCCCAAGAAG AGATTCCAC CAGCCTTACC GGCTTGGGCA 1200

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CGGCCTGATT ACAACCCACC GCTTGTGGAA TCGTGAAGA GGCCAGATTA CCAACCGGCC 1260
 ACTGTTGCGG GCTGCGCTCT CCCCCCCCCT AAGAAAACCC CGACGCCTCC CCCAAGGAGA 1320
 CGCCGGACAG TGGGTCTGAG TGAGAGCTCC ATAGCAGATG CCCTACAACA GCTGGCCATC 1380
 AAGTCCTTTG GCCAGCCCCC CCCAAGCGGC GATTGAGGCC TTTCCACGGG GGCGGACGCA 1440
 GCCGATTCCG GCAGTCGGAC GCCCCCGAT GAGTTGGCCC TTTCCGAGAC AGGTTCCATC 1500
 TCCTCCATGC CCCCTCTCGA GGGGGAGCCT GGAGATCCAG ACTTGAGGCC TGAGCAGGTA 1560
 GAGCTTCAAC CTCCCCCCA GGGGGGGGTG GTAACCCCG GCTCAGGCTC GGGGTCTTGG 1620
 TCTACTTGCT CCGAGGAGGA CGACTCCGTC GTGTGCTGCT CCATGTCATA CTCCTGGACC 1680
 GGGGTCTTAA TAACTCCTTG TAGCCCCGAA GAGGAAAAGT TGCCAATTGG CCCCTTGAGC 1740
 AACTCCCTGT TGCATATCA CAACAAGGTG TACTGTACCA CATCAAAGAG CGCCTCATT 1800
 AGGGTAAAAA AGGTAACCTT TGATAGGATG CAAGCGCTCG ACGCTCATT 1860
 TTGAAGGACA TTAAGCTAGC GGCCTCCAAG GTCACCGCAA GGCTTCTCAC TTTAGAGGAG 1920
 GCCTGCCAGT TAACTCCACC CCACTCTGCA AGATCCAAGT ATGGGTTTGG GGCTAAGGAG 1980
 GTCCGCAGCT TGTCCGGGAG AGCCGTTAAC CACATCAAGT CCGTGTGGAA GGACCTCCTG 2040
 GAAGACACAC AAACACCAAT TCCTACAACC ATCATGGCCA AAAATGAGGT GTTCTGCGTG 2100
 GACCCACCA AGGGGGGTAA GAAAGCAGCT CGCCTTATCG TTTACCCTGA CCTCGGCGTC 2160
 AGGGTCTGCG AGAAAATGGC CCTTTATGAT ATCACACAAA AGCTTCCTCA GGCGGTGATG 2220
 GGGGCTTCTT ATGGATTCCA GACTCCCCC GCTCAGCGGG TGGAGTTTCT CTTGAAGGCA 2280
 TGGGCGGAAA AGAAAGACCC TATGGGTTTT TCGTATGATA CCCGATGCTT TGAACAACC 2340
 GTCCTGAGA GAGACATCAG GACTGAGGAG TCCATATATC GGGCTTGTTT CTTGCCCAG 2400
 GAGGCCACA CTGCCATACA CTCACTGACT GAGAGACTTT ACGTGGGAGG GCCCATGTTT 2460
 AACAGCAAGG GCCAGACCTG CGGGTACAGG CGTTGCCGCG CCAGCGGGGT GCTTACCACT 2520
 AGCATGGGGA ACACCATCAC ATGCTATGTG AAAGCCTTAG CGGCCTGTAA GGCTGCAGGG 2580
 ATAATTGCGC CCACAATGCT GGTATGCGGC GATGACTTGG TTGTCATCTC AGAGAGCCAG 2640
 GGGACCGAGG AGGACGAGCG GAACCTGAGA GCCTTCACGG AGGCTATGAC CAG 2693

Sequence ID No.5
 Sequence Length: 3.033
 Sequence Type: amino acid
 Topology: linear
 Molecule Type: protein

Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr
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Asn	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile
			20						25				30	
Val	Gly	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro	Arg	Leu	Gly
			35						40				45	
Val	Arg	Ala	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser	Gln	Pro	Arg	Gly
			50						55				60	
Arg	Arg	Gln	Pro	Ile	Pro	Lys	Asp	Arg	Arg	Ser	Thr	Gly	Lys	Ser
			65						70				75	
Trp	Gly	Lys	Pro	Gly	Tyr	Pro	Trp	Pro	Leu	Tyr	Gly	Asn	Glu	Gly
			80						85				90	
Leu	Gly	Trp	Ala	Gly	Trp	Leu	Leu	Ser	Pro	Arg	Gly	Ser	Arg	Pro
			95						100				105	
Ser	Trp	Gly	Pro	Asn	Asp	Pro	Arg	His	Arg	Ser	Arg	Asn	Val	Gly
			110						115				120	
Lys	Val	Ile	Asp	Thr	Leu	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly
			125						130				135	
Tyr	Ile	Pro	Val	Val	Gly	Ala	Pro	Leu	Gly	Gly	Val	Ala	Arg	Ala
			140						145				150	
Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Val	Asn	Phe	Ala
			155						160				165	

Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala		
	170	175 180
Leu Leu Ser Cys Ile Thr Thr Pro Val Ser Ala Ala Glu Val Lys		
	185	190 195
Asn Ile Ser Thr Gly Tyr Met Val Thr Asn Asp Cys Thr Asn Asp		
	200	205 210
Ser Ile Thr Trp Gln Leu Gln Ala Ala Val Leu His Val Pro Gly		
	215	220 225
Cys Val Pro Cys Glu Lys Val Gly Asn Thr Ser Arg Cys Trp Ile		
	230	235 240
Pro Val Ser Pro Asn Val Ala Val Gln Gln Pro Gly Ala Leu Thr		
	245	250 255
Gln Gly Leu Arg Thr His Ile Asp Met Val Val Met Ser Ala Thr		
	260	265 270
Leu Cys Ser Ala Leu Tyr Val Gly Asp Leu Cys Gly Gly Val Met		
	275	280 285
Leu Ala Ala Gln Met Phe Ile Val Ser Pro Gln His His Trp Phe		
	290	295 300
Val Gln Asp Cys Asn Cys Ser Ile Tyr Pro Gly Thr Ile Thr Gly		
	305	310 315
His Arg Met Ala Trp Asp Met Met Met Asn Trp Ser Pro Thr Ala		
	320	325 330
Thr Met Ile Leu Ala Tyr Ala Met Arg Val Pro Glu Val Ile Ile		
	335	340 345
Asp Ile Ile Gly Gly Ala His Trp Gly Val Met Phe Gly Leu Ala		
	350	355 360
Tyr Phe Ser Met Gln Gly Ala Trp Ala Lys Val Val Val Ile Leu		
	365	370 375
Leu Leu Ala Ala Gly Val Asp Ala Gln Thr His Thr Val Gly Gly		

	380		385		390
Ser Thr Ala His Asn Ala Arg Thr Leu Thr Gly Met Phe Ser Leu					
	395		400		405
Gly Ala Arg Gln Lys Ile Gln Leu Ile Asn Thr Asn Gly Ser Trp					
	410		415		420
His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu His Thr					
	425		430		435
Gly Phe Leu Ala Ser Leu Phe Tyr Thr His Ser Phe Asn Ser Ser					
	440		445		450
Gly Cys Pro Glu Arg Met Ser Ala Cys Arg Ser Ile Glu Ala Phe					
	455		460		465
Arg Val Gly Trp Gly Ala Leu Gln Tyr Glu Asp Asn Val Thr Asn					
	470		475		480
Pro Glu Asp Met Arg Pro Tyr Cys Trp His Tyr Pro Pro Arg Gln					
	485		490		495
Cys Gly Val Val Ser Ala Ser Ser Val Cys Gly Pro Val Tyr Cys					
	500		505		510
Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Arg Leu Gly					
	515		520		525
Ala Pro Thr Tyr Thr Trp Gly Glu Asn Glu Thr Asp Val Phe Leu					
	530		535		540
Leu Asn Ser Thr Arg Pro Pro Gln Gly Ser Trp Phe Gly Cys Thr					
	545		550		555
Trp Met Asn Ser Thr Gly Tyr Thr Lys Thr Cys Gly Ala Pro Pro					
	560		565		570
Cys Arg Ile Arg Ala Asp Phe Asn Ala Ser Met Asp Leu Leu Cys					
	575		580		585
Pro Thr Asp Cys Phe Arg Lys His Pro Asp Thr Thr Tyr Ile Lys					
	590		595		600

Cys Gly Ser Gly Pro Trp Leu Thr Pro Arg Cys Leu Ile Asp Tyr		
	605	610 615
Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Tyr Thr Ile		
	620	625 630
Phe Lys Ile Arg Met Tyr Val Gly Gly Val Glu His Arg Leu Thr		
	635	640 645
Ala Ala Cys Asn Phe Thr Arg Gly Asp Arg Cys Asn Leu Glu Asp		
	650	655 660
Arg Asp Arg Ser Gln Leu Ser Pro Leu Leu His Ser Thr Thr Glu		
	665	670 675
Trp Ala Ile Leu Pro Cys Thr Tyr Ser Asp Leu Pro Ala Leu Ser		
	680	685 690
Thr Gly Leu Leu His Leu His Gln Asn Ile Val Asp Val Gln Phe		
	695	700 705
Met Tyr Gly Leu Ser Pro Ala Leu Thr Lys Tyr Ile Val Arg Trp		
	710	715 720
Glu Trp Val Val Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Val		
	725	730 735
Cys Ala Cys Leu Trp Met Leu Ile Leu Leu Gly Gln Ala Glu Ala		
	740	745 750
Ala Leu Glu Lys Leu Val Val Leu His Ala Ala Ser Ala Ala Ser		
	755	760 765
Cys Asn Gly Phe Leu Tyr Phe Val Ile Phe Phe Val Ala Ala Trp		
	770	775 780
Tyr Ile Lys Gly Arg Val Val Pro Leu Ala Thr Tyr Ser Leu Thr		
	785	790 795
Gly Leu Trp Ser Phe Gly Leu Leu Leu Leu Ala Leu Pro Gln Gln		
	800	805 810
Ala Tyr Ala Tyr Asp Ala Ser Val His Gly Gln Ile Gly Ala Ala		

815	820	825
Leu Leu Val Leu Ile Thr Leu Phe Thr	Leu Thr Pro Gly Tyr Lys	
830	835	840
Thr Leu Leu Ser Arg Phe Leu Trp Trp	Leu Cys Tyr Leu Leu Thr	
845	850	855
Leu Ala Glu Ala Met Val Gln Glu Trp	Ala Pro Pro Met Gln Val	
860	865	870
Arg Gly Gly Arg Asp Gly Ile Ile Trp	Ala Val Ala Ile Phe Cys	
875	880	885
Pro Gly Val Val Phe Asp Ile Thr Lys	Trp Leu Leu Ala Val Leu	
890	895	900
Gly Pro Ala Tyr Leu Leu Lys Gly Ala	Leu Thr Arg Val Pro Tyr	
905	910	915
Phe Val Arg Ala His Ala Leu Leu Arg	Met Cys Thr Met Val Arg	
920	925	930
His Leu Ala Gly Gly Arg Tyr Val Gln	Met Val Leu Leu Ala Leu	
935	940	945
Gly Arg Trp Thr Gly Thr Tyr Ile Tyr	Asp His Leu Thr Pro Met	
950	955	960
Ser Asp Trp Ala Ala Asn Gly Leu Arg	Asp Leu Ala Val Ala Val	
965	970	975
Glu Pro Ile Ile Phe Ser Pro Met Glu	Lys Lys Val Ile Val Trp	
980	985	990
Gly Ala Glu Thr Ala Ala Cys Gly Asp	Ile Leu His Gly Leu Pro	
995	1000	1005
Val Ser Ala Arg Leu Gly Arg Glu Val	Leu Leu Gly Pro Ala Asp	
1010	1015	1020
Gly Tyr Thr Ser Lys Gly Trp Ser Leu	Leu Ala Pro Ile Thr Ala	
1025	1030	1035

Tyr Ala Gln Gln Thr Arg Gly Leu Leu Gly Thr Ile Val Val Ser			
	1040	1045	1050
Met Thr Gly Arg Asp Lys Thr Glu Gln Ala Gly Glu Ile Glu Val			
	1055	1060	1065
Leu Ser Thr Val Thr Gln Ser Phe Leu Gly Thr Thr Ile Ser Gly			
	1070	1075	1080
Val Leu Trp Thr Val Tyr His Gly Ala Gly Asn Lys Thr Leu Ala			
	1085	1090	1095
Gly Ser Arg Gly Pro Val Thr Gln Met Tyr Ser Ser Ala Glu Gly			
	1100	1105	1110
Asp Leu Val Gly Trp Pro Ser Pro Pro Gly Thr Lys Ser Leu Glu			
	1115	1120	1125
Pro Cys Thr Cys Gly Ala Val Asp Leu Tyr Leu Val Thr Arg Asn			
	1130	1135	1140
Ala Asp Val Ile Pro Ala Arg Arg Arg Gly Asp Lys Arg Gly Ala			
	1145	1150	1155
Leu Leu Ser Pro Arg Pro Leu Ser Thr Leu Lys Gly Ser Ser Gly			
	1160	1165	1170
Gly Pro Val Leu Cys Pro Arg Gly His Ala Val Gly Val Phe Arg			
	1175	1180	1185
Ala Ala Val Cys Ser Arg Gly Val Ala Lys Ser Ile Asp Phe Ile			
	1190	1195	1200
Pro Val Glu Thr Leu Asp Ile Val Thr Arg Ser Pro Thr Phe Ser			
	1205	1210	1215
Asp Asn Ser Thr Pro Pro Ala Val Pro Gln Thr Tyr Gln Val Gln			
	1220	1225	1230
Tyr Leu His Ala Pro Thr Gly Ser Gly Lys Ser Thr Lys Val Pro			
	1235	1240	1245
Val Ala Tyr Ala Ala Gln Gly Tyr Lys Val Leu Val Leu Asn Pro			

1250	1255	1260
Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr Leu Ser Lys Ala		
1265	1270	1275
His Gly Ile Asn Pro Asn Ile Arg Thr Gly Val Arg Thr Val Thr		
1280	1285	1290
Thr Gly Ala Pro Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Leu Ala		
1295	1300	1305
Asp Gly Gly Cys Ala Gly Gly Ala Tyr Asp Ile Ile Ile Cys Asp		
1310	1315	1320
Glu Cys His Ala Val Asp Ser Thr Thr Ile Leu Gly Ile Gly Thr		
1325	1330	1335
Val Leu Asp Gln Ala Glu Thr Ala Gly Val Arg Leu Thr Val Leu		
1340	1345	1350
Ala Thr Ala Thr Pro Pro Gly Ser Val Thr Thr Pro His Pro Asn		
1355	1360	1365
Ile Glu Glu Val Ala Leu Gly Gln Glu Gly Glu Ile Pro Phe Tyr		
1370	1375	1380
Gly Arg Ala Ile Pro Leu Ser Tyr Ile Lys Gly Gly Arg His Leu		
1385	1390	1395
Ile Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Ala		
1400	1405	1410
Leu Arg Gly Met Gly Leu Asn Ala Val Ala Tyr Tyr Arg Gly Leu		
1415	1420	1425
Asp Val Ser Val Ile Pro Thr Gln Gly Asp Val Val Val Val Ala		
1430	1435	1440
Thr Asp Ala Leu Met Thr Gly Phe Thr Gly Asp Phe Asp Ser Val		
1445	1450	1455
Ile Asp Cys Asn Val Ala Val Thr Gln Val Val Asp Phe Ser Leu		
1460	1465	1470

Asp Pro Thr Phe Thr Ile Thr Thr Gln Thr Val Pro Gln Asp Ala	1475	1480	1485
Val Ser Arg Ser Gln Arg Arg Gly Arg Thr Gly Arg Gly Arg Leu	1490	1495	1500
Gly Ile Tyr Arg Tyr Val Ser Thr Gly Glu Arg Ala Ser Gly Met	1505	1510	1515
Phe Asp Ser Val Val Leu Cys Glu Cys Tyr Asp Ala Gly Ala Ala	1520	1525	1530
Trp Tyr Glu Leu Thr Pro Ala Glu Thr Thr Val Arg Leu Arg Ala	1535	1540	1545
Tyr Phe Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu Glu	1550	1555	1560
Phe Trp Glu Ala Val Phe Thr Gly Leu Thr His Ile Asp Ala His	1565	1570	1575
Phe Leu Ser Gln Thr Lys Gln Ser Gly Glu Asn Phe Ala Tyr Leu	1580	1585	1590
Thr Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Lys Ala Pro Pro	1595	1600	1605
Pro Ser Trp Asp Val Met Trp Lys Cys Leu Thr Arg Leu Lys Pro	1610	1615	1620
Trp Leu Val Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ser Val	1625	1630	1635
Thr Asn Glu Val Thr Leu Thr His Pro Val Thr Lys Tyr Ile Ala	1640	1645	1650
Thr Cys Met Gln Ala Asp Leu Glu Val Met Thr Ser Thr Trp Val	1655	1660	1665
Leu Ala Gly Gly Val Leu Ala Ala Val Ala Ala Tyr Cys Leu Ala	1670	1675	1680
Thr Gly Cys Val Cys Ile Ile Gly Arg Leu His Val Asn Gln Arg			

1685	1690	1695
Ala Val Val Ala Pro Asp Lys Glu Val Leu Tyr Glu Ala Phe Asp		
1700	1705	1710
Glu Met Glu Glu Cys Ala Ser Arg Ala Ala Leu Ile Glu Glu Gly		
1715	1720	1725
Gln Arg Ile Ala Glu Met Leu Lys Ser Lys Ile Gln Gly Leu Leu		
1730	1735	1740
Gln Gln Ala Ser Lys Gln Ala Gln Asp Ile Gln Pro Ala Val Gln		
1745	1750	1755
Ala Ser Trp Pro Lys Val Glu Gln Phe Trp Ala Lys His Met Trp		
1760	1765	1770
Asn Phe Ile Ser Gly Ile Gln Tyr Leu Ala Gly Leu Ser Thr Leu		
1775	1780	1785
Pro Gly Asn Pro Ala Val Ala Ser Met Met Ala Phe Ser Ala Ala		
1790	1795	1800
Leu Thr Ser Pro Leu Ser Thr Ser Thr Thr Ile Leu Leu Asn Ile		
1805	1810	1815
Leu Gly Gly Trp Leu Ala Ser Gln Ile Ala Pro Pro Ala Gly Ala		
1820	1825	1830
Thr Gly Phe Val Val Ser Gly Leu Val Gly Ala Ala Val Gly Ser		
1835	1840	1845
Ile Gly Leu Gly Lys Val Leu Val Asp Ile Leu Ala Gly Tyr Gly		
1850	1855	1860
Ala Gly Ile Ser Gly Ala Leu Val Ala Phe Lys Ile Met Ser Gly		
1865	1870	1875
Glu Lys Pro Ser Met Glu Asp Val Val Asn Leu Leu Pro Gly Ile		
1880	1885	1890
Leu Ser Pro Gly Ala Leu Val Val Gly Val Ile Cys Ala Ala Ile		
1895	1900	1905

Leu Arg Arg His Val Gly Pro Gly Glu Gly Ala Val Gln Trp Met		
1910	1915	1920
Asn Arg Leu Ile Ala Phe Ala Ser Arg Gly Asn His Val Ala Pro		
1925	1930	1935
Thr His Tyr Val Thr Glu Ser Asp Ala Ser Gln Arg Val Thr Gln		
1940	1945	1950
Leu Leu Gly Ser Leu Thr Ile Thr Ser Leu Leu Arg Arg Leu His		
1955	1960	1965
Asn Trp Ile Thr Glu Asp Cys Pro Ile Pro Cys Ser Gly Ser Trp		
1970	1975	1980
Leu Arg Asp Val Trp Asp Trp Val Cys Thr Ile Leu Thr Asp Phe		
1985	1990	1995
Lys Asn Trp Leu Thr Ser Lys Leu Phe Pro Lys Met Pro Gly Leu		
2000	2005	2010
Pro Phe Ile Ser Cys Gln Lys Gly Tyr Lys Gly Val Trp Ala Gly		
2015	2020	2025
Thr Gly Ile Met Thr Thr Arg Cys Pro Cys Gly Ala Asn Ile Ser		
2030	2035	2040
Gly Asn Val Arg Leu Gly Ser Met Arg Ile Thr Gly Pro Lys Thr		
2045	2050	2055
Cys Met Asn Ile Trp Gln Gly Thr Phe Pro Ile Asn Cys Tyr Thr		
2060	2065	2070
Glu Gly Gln Cys Val Pro Lys Pro Ala Pro Asn Phe Lys Ile Ala		
2075	2080	2085
Ile Trp Arg Val Ala Ala Ser Glu Tyr Ala Glu Val Thr Gln His		
2090	2095	2100
Gly Ser Tyr His Tyr Ile Thr Gly Leu Thr Thr Asp Asn Leu Lys		
2105	2110	2115
Val Pro Cys Gln Leu Pro Ser Pro Glu Phe Phe Ser Trp Val Asp		

2120	2125	2130
Gly Val Gln Ile His Arg Phe Ala Pro Ile Pro Lys Pro Phe Phe		
2135	2140	2145
Arg Asp Glu Val Ser Phe Cys Val Gly Leu Asn Ser Phe Val Val		
2150	2155	2160
Gly Ser Gln Leu Pro Cys Asp Pro Glu Pro Asp Thr Asp Val Leu		
2165	2170	2175
Thr Ser Met Leu Thr Asp Pro Ser His Ile Thr Ala Glu Thr Ala		
2180	2185	2190
Ala Arg Arg Leu Ala Arg Gly Ser Pro Pro Ser Glu Ala Ser Ser		
2195	2200	2205
Ser Ala Ser Gln Leu Ser Ala Pro Ser Leu Arg Ala Thr Cys Thr		
2210	2215	2220
Thr His Gly Lys Ala Tyr Asp Val Asp Met Val Asp Ala Asn Leu		
2225	2230	2235
Phe Met Gly Gly Asp Val Thr Arg Ile Glu Ser Glu Ser Lys Val		
2240	2245	2250
Val Val Leu Asp Ser Leu Asp Pro Met Val Glu Glu Arg Ser Asp		
2255	2260	2265
Leu Glu Pro Ser Ile Pro Ser Glu Tyr Met Leu Pro Lys Lys Arg		
2270	2275	2280
Phe Pro Pro Ala Leu Pro Ala Trp Ala Arg Pro Asp Tyr Asn Pro		
2285	2290	2295
Pro Leu Val Glu Ser Trp Lys Arg Pro Asp Tyr Gln Pro Ala Thr		
2300	2305	2310
Val Ala Gly Cys Ala Leu Pro Pro Pro Lys Lys Thr Pro Thr Pro		
2315	2320	2325
Pro Pro Arg Arg Arg Arg Thr Val Gly Leu Ser Glu Ser Ser Ile		
2330	2335	2340

Ala Asp Ala Leu Gln Gln Leu Ala Ile Lys Ser Phe Gly Gln Pro			
	2345	2350	2355
Pro Pro Ser Gly Asp Ser Gly Leu Ser Thr Gly Ala Asp Ala Ala			
	2360	2365	2370
Asp Ser Gly Ser Arg Thr Pro Pro Asp Glu Leu Ala Leu Ser Glu			
	2375	2380	2385
Thr Gly Ser Ile Ser Ser Met Pro Pro Leu Glu Gly Glu Pro Gly			
	2390	2395	2400
Asp Pro Asp Leu Glu Pro Glu Gln Val Glu Leu Gln Pro Pro Pro			
	2405	2410	2415
Gln Gly Gly Val Val Thr Pro Gly Ser Gly Ser Gly Ser Trp Ser			
	2420	2425	2430
Thr Cys Ser Glu Glu Asp Asp Ser Val Val Cys Cys Ser Met Ser			
	2435	2440	2445
Tyr Ser Trp Thr Gly Ala Leu Ile Thr Pro Cys Ser Pro Glu Glu			
	2450	2455	2460
Glu Lys Leu Pro Ile Asn Pro Leu Ser Asn Ser Leu Leu Arg Tyr			
	2465	2470	2475
His Asn Lys Val Tyr Cys Thr Thr Ser Lys Ser Ala Ser Leu Arg			
	2480	2485	2490
Ala Lys Lys Val Thr Phe Asp Arg Met Gln Ala Leu Asp Ala His			
	2495	2500	2505
Tyr Asp Ser Val Leu Lys Asp Ile Lys Leu Ala Ala Ser Lys Val			
	2510	2515	2520
Thr Ala Arg Leu Leu Thr Leu Glu Glu Ala Cys Gln Leu Thr Pro			
	2525	2530	2535
Pro His Ser Ala Arg Ser Lys Tyr Gly Phe Gly Ala Lys Glu Val			
	2540	2545	2550

Arg Ser Leu Ser Gly Arg Ala Val Asn His Ile Lys Ser Val Trp			
	2555	2560	2565
Lys Asp Leu Leu Glu Asp Thr Gln Thr Pro Ile Pro Thr Thr Ile			
	2570	2575	2580
Met Ala Lys Asn Glu Val Phe Cys Val Asp Pro Thr Lys Gly Gly			
	2585	2590	2595
Lys Lys Ala Ala Arg Leu Ile Val Tyr Pro Asp Leu Gly Val Arg			
	2600	2605	2610
Val Cys Glu Lys Met Ala Leu Tyr Asp Ile Thr Gln Lys Leu Pro			
	2615	2620	2625
Gln Ala Val Met Gly Ala Ser Tyr Gly Phe Gln Tyr Ser Pro Ala			
	2630	2635	2640
Gln Arg Val Glu Phe Leu Leu Lys Ala Trp Ala Glu Lys Lys Asp			
	2645	2650	2655
Pro Met Gly Phe Ser Tyr Asp Thr Arg Cys Phe Asp Ser Thr Val			
	2660	2665	2670
Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr Arg Ala Cys			
	2675	2680	2685
Ser Leu Pro Glu Glu Ala His Thr Ala Ile His Ser Leu Thr Glu			
	2690	2695	2700
Arg Leu Tyr Val Gly Gly Pro Met Phe Asn Ser Lys Gly Gln Thr			
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Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Leu Thr Thr Ser			
	2720	2725	2730
Met Gly Asn Thr Ile Thr Cys Tyr Val Lys Ala Leu Ala Ala Cys			
	2735	2740	2745
Lys Ala Ala Gly Ile Ile Ala Pro Thr Met Leu Val Cys Gly Asp			
	2750	2755	2760

Asp Leu Val Val Ile Ser Glu Ser Gln Gly Thr Glu Glu Asp Glu			
	2765	2770	2775
Arg Asn Leu Arg Ala Phe Thr Glu Ala Met Thr Arg Tyr Ser Ala			
	2780	2785	2790
Pro Pro Gly Asp Pro Pro Arg Pro Glu Tyr Asp Leu Glu Leu Ile			
	2795	2800	2805
Thr Ser Cys Ser Ser Asn Val Ser Val Ala Leu Gly Pro Gln Gly			
	2810	2815	2820
Arg Arg Arg Tyr Tyr Leu Thr Arg Asp Pro Thr Thr Pro Ile Ala			
	2825	2830	2835
Arg Ala Ala Trp Glu Thr Val Arg His Ser Pro Val Asn Ser Trp			
	2840	2845	2850
Leu Gly Asn Ile Ile Gln Tyr Ala Pro Thr Ile Trp Ala Arg Met			
	2855	2860	2865
Val Leu Met Thr His Phe Phe Ser Ile Leu Met Ala Gln Asp Thr			
	2870	2875	2880
Leu Asp Gln Asn Leu Asn Phe Glu Met Tyr Gly Ala Val Tyr Ser			
	2885	2890	2895
Val Ser Pro Leu Asp Leu Pro Ala Ile Ile Glu Arg Leu His Gly			
	2900	2905	2910
Leu Asp Ala Phe Ser Leu His Thr Tyr Thr Pro His Glu Leu Thr			
	2915	2920	2925
Arg Val Ala Ser Ala Leu Arg Lys Leu Gly Ala Pro Pro Leu Arg			
	2930	2935	2940
Ala Trp Lys Ser Arg Ala Arg Ala Val Arg Ala Ser Leu Ile Ser			
	2945	2950	2955
Arg Gly Gly Arg Ala Ala Val Cys Gly Arg Tyr Leu Phe Asn Trp			
	2960	2965	2970

Ala Val Lys Thr Lys Leu Lys Leu Thr Pro Leu Pro Glu Ala Arg		
	2975	2980 2985
Leu Leu Asp Leu Ser Ser Trp Phe Thr Val Gly Ala Gly Gly Gly		
	2990	2995 3000
Asp Ile Tyr His Ser Val Ser Arg Ala Arg Pro Arg Leu Leu Leu		
	3005	3010 3015
Leu Gly Leu Leu Leu Leu Phe Val Gly Val Gly Leu Phe Leu Leu		
	3020	3025 3030
Pro Ala Arg		
	3033	

Sequence ID No. **6**
Sequence Length: 9,511
Sequence Type: nucleic acid
Strandedness: single
Topology: linear
Molecule Type: genomic RNA
Method for Determination of Feature: E

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GCCCCCCCC UGAUGGGGGC GACACUCCGC CAUGAAUCAC UCCCCUGUGA GGAACUACUG   60
UCUUCACGCA GAAAGCGUCU AGCCAUGGCG UUAGUAUGAG UGUCGUACAG CCUCCAGGCC  120
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 TAGTGGTYTT GGCCACAGCC ACGCCTCCCG GTACGGTGAC AACTCCCCAC AGTAACATAG 4440
 AGGAGGTGGC CCTTGGTCAC GAGGGCGAGA TCCCTTTTTA TGGCAAAGCT ATTCCCCTAG 4500
 CTTTCATCAA GGGGGGCGA CACTTGATCT TTTGCCATT AAAGAAGAAG TGCGACGAGC 4560
 TCGCAGCGGC CCTCCGGGGC AYGGGTGTCA ATGCCGTTGC ATACTATAGG GGTCTCGACG 4620
 TCTCCGTTAT ACCAACTCAA GGAGACGTGG TGGTTGTCGC CACTGATGCC CTAATGACTG 4680

GGTACACCGG CGACTTTGAC TCYGTCAATG ACTGTAATGT TGCAGTCTCT CAGATTGTTG 4740
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 CCGGGGCAGC CTGGTACGAG CTTACACCTG CTGAGACTAC GGTGAGACTC CGGGCYTATT 4980
 TCAACACGCC CGGTTTGCCC GTATGTCAAG ACCACCTGGA GTTCTGGGAA GCGGTCTTTA 5040
 CAGGTCTCAC WCACATTRAC GCCCACTTCC TCTCCAGAC GAAGCAAGGA GGAGAAAAC 5100
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 CCTCCTGTA CCGCTTGGGT GCCGTGACCA ATGAGGTYAC CTTGACGCAC CCCGTGACGA 5280
 AATACATCGC CACGTGCATG CAAGCTGACC TYGAGATCAT GACAAGCTCA TGGGTCCTGG 5340
 CGGGGGGGGT GCTAGCCGCC GTGGCAGCTT ACTGCCTGGC GACTGGCTGC ATTTCCATCA 5400
 TTGGCCGCTT ACACCTGAAT GATCGGGTGG TTGTGRCCCC YGACAAGGAR ATCTTATATG 5460
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 CGCATGCYCG ACCCGCCTA TTAATCCTTT GCCTACTCCT ACTTAGCGTA GGAGTAGGCA 9420
 TCTTTTACT CCCCCTCGG TAGAGCGGCA AACYCTAGCT AACTCCATA GCTAGTTTCC 9480
 GTTTTTTTT TTTTTTTTT TTTTTTTTT T 9511

Sequence ID No. 8
 Sequence Length: 3,033
 Sequence Type: amino acid
 Topology: linear
 Molecule Type: protein

Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr
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Asn	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile
				20					25					30
Val	Gly	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro	Arg	Leu	Gly
				35					40					45
Val	Arg	Ala	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser	Gln	Pro	Arg	Gly
				50					55					60
Arg	Arg	Gln	Pro	Ile	Pro	Lys	Asp	Arg	Arg	Ser	Thr	Gly	Lys	Ser
				65					70					75
Trp	Gly	Lys	Pro	Gly	Tyr	Pro	Trp	Pro	Leu	Tyr	Gly	Asn	Glu	Gly
				80					85					90
Cys	Gly	Trp	Ala	Gly	Trp	Leu	Leu	Ser	Pro	Arg	Gly	Ser	Arg	Pro
				95					100					105
Thr	Trp	Gly	Pro	Thr	Asp	Pro	Arg	His	Arg	Ser	Arg	Asn	Leu	Gly
				110					115					120
Arg	Val	Ile	Asp	Thr	Ile	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly
				125					130					135
Tyr	Ile	Pro	Val	Val	Gly	Ala	Pro	Val	Gly	Gly	Val	Ala	Arg	Ala
				140					145					150
Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Ile	Asn	Tyr	Ala
				155					160					165

Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala		
	170	175 180
Leu Leu Ser Cys Val Thr Val Pro Val Ser Ala Val Glu Val Arg		
	185	190 195
Asn Ile Ser Ser Ser Tyr Tyr Ala Thr Asn Asp Cys Ser Asn Asn		
	200	205 210
Ser Ile Thr Trp Gln Leu Thr Asp Ala Val Leu His Leu Pro Gly		
	215	220 225
Cys Val Pro Cys Glu Asn Asp Asn Gly Thr Leu His Cys Trp Ile		
	230	235 240
Gln Val Thr Pro Asn Val Ala Val Lys His Arg Gly Ala Leu Thr		
	245	250 255
Arg Ser Leu Arg Thr His Val Asp Met Ile Val Met Ala Ala Thr		
	260	265 270
Ala Cys Ser Ala Leu Tyr Val Gly Asp Val Cys Gly Ala Val Met		
	275	280 285
Ile Leu Ser Gln Ala Phe Met Val Ser Pro Gln Arg His Asn Phe		
	290	295 300
Thr Gln Glu Cys Asn Cys Ser Ile Tyr Gln Gly His Ile Thr Gly		
	305	310 315
His Arg Met Ala Trp Asp Met Met Leu Ser Trp Ser Pro Thr Leu		
	320	325 330
Thr Met Ile Leu Ala Tyr Ala Ala Arg Val Pro Glu Leu Val Leu		
	335	340 345
Glu Ile Ile Phe Gly Gly His Trp Gly Val Val Phe Gly Leu Ala		
	350	355 360
Tyr Phe Ser Met Gln Gly Ala Trp Ala Lys Val Ile Ala Ile Leu		
	365	370 375
Leu Leu Val Ala Gly Val Asp Ala Thr Thr Tyr Ser Ser Gly Gln		

	380		385		390
Glu Ala Gly Arg Thr Val Ala Gly Phe Ala Gly Leu Phe Thr Thr					
	395		400		405
Gly Ala Lys Gln Asn Leu Tyr Leu Ile Asn Thr Asn Gly Ser Trp					
	410		415		420
His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Gln Thr					
	425		430		435
Gly Phe Leu Ala Ser Leu Phe Tyr Thr His Lys Phe Asn Ser Ser					
	440		445		450
Gly Cys Pro Glu Arg Leu Ser Ser Cys Arg Gly Leu Asp Asp Phe					
	455		460		465
Arg Ile Gly Trp Gly Thr Leu Glu Tyr Glu Thr Asn Val Thr Asn					
	470		475		480
Asp Gly Asp Met Arg Pro Tyr Cys Trp His Tyr Pro Pro Arg Pro					
	485		490		495
Cys Gly Ile Val Pro Ala Arg Thr Val Cys Gly Pro Val Tyr Cys					
	500		505		510
Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Lys Gln Gly					
	515		520		525
Val Pro Thr Tyr Thr Trp Gly Glu Asn Glu Thr Asp Val Phe Leu					
	530		535		540
Leu Asn Ser Thr Arg Pro Pro Arg Gly Ala Trp Phe Gly Cys Thr					
	545		550		555
Trp Met Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Ala Pro Pro					
	560		565		570
Cys Arg Ile Arg Lys Asp Tyr Asn Ser Thr Ile Asp Leu Leu Cys					
	575		580		585
Pro Thr Asp Cys Phe Arg Lys His Pro Asp Ala Thr Tyr Leu Lys					
	590		595		600

Cys Gly Ala Gly Pro Trp Leu Thr Pro Arg Cys Leu Val Asp Tyr		
	605	610 615
Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile		
	620	625 630
Phe Lys Ala Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Ser		
	635	640 645
Ala Ala Cys Asn Phe Thr Arg Gly Asp Arg Cys Arg Leu Glu Asp		
	650	655 660
Arg Asp Arg Gly Gln Gln Ser Pro Leu Leu His Ser Thr Thr Glu		
	665	670 675
Trp Ala Val Leu Pro Cys Ser Phe Ser Asp Leu Pro Ala Leu Ser		
	680	685 690
Thr Gly Leu Leu His Leu His Gln Asn Ile Val Asp Val Gln Tyr		
	695	700 705
Leu Tyr Gly Leu Ser Pro Ala Leu Thr Arg Tyr Ile Val Lys Trp		
	710	715 720
Glu Trp Val Ile Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Ile		
	725	730 735
Cys Ala Cys Leu Trp Met Leu Ile Ile Leu Gly Gln Ala Glu Ala		
	740	745 750
Ala Leu Glu Lys Leu Ile Ile Leu His Ser Ala Ser Ala Ala Ser		
	755	760 765
Ala Asn Gly Pro Leu Trp Phe Phe Ile Phe Phe Thr Ala Ala Trp		
	770	775 780
Tyr Leu Lys Gly Arg Val Val Pro Val Ala Thr Tyr Ser Val Leu		
	785	790 795
Gly Leu Trp Ser Phe Leu Leu Leu Val Leu Ala Leu Pro Gln Gln		
	800	805 810
Ala Tyr Ala Leu Asp Ala Ala Glu Gln Gly Glu Leu Gly Leu Ala		

815	820	825
Ile Leu Val Ile Ile Ser Ile Phe Thr Leu Thr Pro Ala Tyr Lys		
830	835	840
Ile Leu Leu Ser Arg Ser Val Trp Trp Leu Ser Tyr Met Leu Val		
845	850	855
Leu Ala Glu Ala Gln Ile Gln Gln Trp Val Pro Pro Leu Glu Val		
860	865	870
Arg Gly Gly Arg Asp Gly Ile Ile Trp Val Ala Val Ile Leu His		
875	880	885
Pro Arg Leu Val Phe Glu Val Thr Lys Trp Leu Leu Ala Ile Leu		
890	895	900
Gly Pro Ala Tyr Leu Leu Lys Ala Ser Leu Leu Arg Ile Pro Tyr		
905	910	915
Phe Val Arg Ala His Ala Leu Leu Arg Val Cys Thr Leu Val Lys		
920	925	930
His Leu Ala Gly Ala Arg Tyr Ile Gln Met Leu Leu Ile Thr Ile		
935	940	945
Gly Arg Trp Thr Gly Thr Tyr Ile Tyr Asp His Leu Ser Pro Leu		
950	955	960
Ser Thr Trp Ala Ala Gln Gly Leu Arg Asp Leu Ala Ile Ala Val		
965	970	975
Glu Pro Val Val Phe Ser Pro Met Glu Lys Lys Val Ile Val Trp		
980	985	990
Gly Ala Glu Thr Val Ala Cys Gly Asp Ile Leu His Gly Leu Pro		
995	1000	1005
Val Ser Ala Arg Leu Gly Arg Glu Val Leu Leu Gly Pro Ala Asp		
1010	1015	1020
Gly Tyr Thr Ser Lys Gly Trp Lys Leu Leu Ala Pro Ile Thr Ala		
1025	1030	1035

Tyr Thr Gln Gln Thr Arg Gly Leu Leu Gly Ala Ile Val Val Ser			
	1040	1045	1050
Leu Thr Gly Arg Asp Lys Asn Glu Gln Ala Gly Gln Val Gln Val			
	1055	1060	1065
Leu Ser Ser Val Thr Gln Thr Phe Leu Gly Thr Ser Ile Ser Gly			
	1070	1075	1080
Val Leu Trp Thr Val Tyr His Gly Ala Gly Asn Lys Thr Leu Ala			
	1085	1090	1095
Gly Pro Lys Gly Pro Val Thr Gln Met Tyr Thr Ser Ala Glu Gly			
	1100	1105	1110
Asp Leu Val Gly Trp Pro Ser Pro Pro Gly Thr Lys Ser Leu Asp			
	1115	1120	1125
Pro Cys Thr Cys Gly Ala Val Asp Leu Tyr Leu Val Thr Arg Asn			
	1130	1135	1140
Ala Asp Val Ile Pro Val Arg Arg Lys Asp Asp Arg Arg Gly Ala			
	1145	1150	1155
Leu Leu Ser Pro Arg Pro Leu Ser Thr Leu Lys Gly Ser Ser Gly			
	1160	1165	1170
Gly Pro Val Leu Cys Ser Arg Gly His Ala Val Gly Leu Phe Arg			
	1175	1180	1185
Ala Ala Val Cys Ala Arg Gly Val Ala Lys Ser Ile Asp Phe Ile			
	1190	1195	1200
Pro Val Glu Ser Leu Asp Val Ala Thr Arg Thr Pro Ser Phe Ser			
	1205	1210	1215
Asp Asn Ser Thr Pro Pro Ala Val Pro Gln Ser Tyr Gln Val Gly			
	1220	1225	1230
Tyr Leu His Ala Pro Thr Gly Ser Gly Lys Ser Thr Lys Val Pro			
	1235	1240	1245
Ala Ala Tyr Ala Ser Gln Gly Tyr Lys Val Leu Val Leu Asn Pro			

1250	1255	1260
Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr Met Ser Lys Ala		
1265	1270	1275
His Gly Ile Asn Pro Asn Ile Arg Thr Gly Val Arg Thr Val Thr		
1280	1285	1290
Thr Gly Asp Ser Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Ile Ala		
1295	1300	1305
Asp Gly Gly Cys Ala Ala Gly Ala Tyr Asp Ile Ile Ile Cys Asp		
1310	1315	1320
Glu Cys His Ser Val Asp Ala Thr Thr Ile Leu Gly Ile Gly Thr		
1325	1330	1335
Val Leu Asp Gln Ala Glu Thr Ala Gly Val Arg Leu Val Val Leu		
1340	1345	1350
Ala Thr Ala Thr Pro Pro Gly Thr Val Thr Thr Pro His Ser Asn		
1355	1360	1365
Ile Glu Glu Val Ala Leu Gly His Glu Gly Glu Ile Pro Phe Tyr		
1370	1375	1380
Gly Lys Ala Ile Pro Leu Ala Phe Ile Lys Gly Gly Arg His Leu		
1385	1390	1395
Ile Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Ala		
1400	1405	1410
Leu Arg Gly Met Gly Val Asn Ala Val Ala Tyr Tyr Arg Gly Leu		
1415	1420	1425
Asp Val Ser Val Ile Pro Thr Gln Gly Asp Val Val Val Val Ala		
1430	1435	1440
Thr Asp Ala Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val		
1445	1450	1455
Ile Asp Cys Asn Val Ala Val Ser Gln Ile Val Asp Phe Ser Leu		
1460	1465	1470

Asp Pro Thr Phe Thr Ile Thr Thr Gln Thr Val Pro Gln Asp Ala		
	1475	1485
Val Ser Arg Ser Gln Arg Arg Gly Arg Thr Gly Arg Gly Arg Leu		
	1490	1500
Gly Val Tyr Arg Tyr Val Ser Ser Gly Glu Arg Pro Ser Gly Met		
	1505	1515
Phe Asp Ser Val Val Leu Cys Glu Cys Tyr Asp Ala Gly Ala Ala		
	1520	1530
Trp Tyr Glu Leu Thr Pro Ala Glu Thr Thr Val Arg Leu Arg Ala		
	1535	1545
Tyr Phe Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu Glu		
	1550	1560
Phe Trp Glu Ala Val Phe Thr Gly Leu Thr His Ile Asp Ala His		
	1565	1575
Phe Leu Ser Gln Thr Lys Gln Gly Gly Glu Asn Phe Ala Tyr Leu		
	1580	1590
Thr Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Lys Ala Pro Pro		
	1595	1605
Pro Ser Trp Asp Val Met Trp Lys Cys Leu Thr Arg Leu Lys Pro		
	1610	1620
Thr Leu Thr Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val		
	1625	1635
Thr Asn Glu Val Thr Leu Thr His Pro Val Thr Lys Tyr Ile Ala		
	1640	1650
Thr Cys Met Gln Ala Asp Leu Glu Ile Met Thr Ser Ser Trp Val		
	1655	1665
Leu Ala Gly Gly Val Leu Ala Ala Val Ala Ala Tyr Cys Leu Ala		
	1670	1680
Thr Gly Cys Ile Ser Ile Ile Gly Arg Leu His Leu Asn Asp Arg		

1685	1690	1695
Val Val Val Ala Pro Asp Lys Glu Ile Leu Tyr Glu Ala Phe Asp		
1700	1705	1710
Glu Met Glu Glu Cys Ala Ser Lys Ala Ala Leu Ile Glu Glu Gly		
1715	1720	1725
Gln Arg Met Ala Glu Met Leu Lys Ser Lys Ile Gln Gly Leu Leu		
1730	1735	1740
Gln Gln Ala Thr Arg Gln Ala Gln Asp Ile Gln Pro Ala Ile Gln		
1745	1750	1755
Ser Ser Trp Pro Lys Leu Glu Gln Phe Trp Ala Lys His Met Trp		
1760	1765	1770
Asn Phe Ile Ser Gly Ile Gln Tyr Leu Ala Gly Leu Ser Thr Leu		
1775	1780	1785
Pro Gly Asn Pro Ala Val Ala Ser Met Met Ala Phe Ser Ala Ala		
1790	1795	1800
Leu Thr Ser Pro Leu Pro Thr Ser Thr Thr Ile Leu Leu Asn Ile		
1805	1810	1815
Met Gly Gly Trp Leu Ala Ser Gln Ile Ala Pro Pro Ala Gly Ala		
1820	1825	1830
Thr Gly Phe Val Val Ser Gly Leu Val Gly Ala Ala Val Gly Ser		
1835	1840	1845
Ile Gly Leu Gly Lys Ile Leu Val Asp Val Leu Ala Gly Tyr Gly		
1850	1855	1860
Ala Gly Ile Ser Gly Ala Leu Val Ala Phe Lys Ile Met Ser Gly		
1865	1870	1875
Glu Lys Pro Thr Val Glu Asp Val Val Asn Leu Leu Pro Ala Ile		
1880	1885	1890
Leu Ser Pro Gly Ala Leu Val Val Gly Val Ile Cys Ala Ala Ile		
1895	1900	1905

Leu Arg Arg His Val Gly Gln Gly Glu Gly Ala Val Gln Trp Met		
1910	1915	1920
Asn Arg Leu Ile Ala Phe Ala Ser Arg Gly Asn His Val Ala Pro		
1925	1930	1935
Thr His Tyr Val Val Glu Ser Asp Ala Ser Gln Arg Val Thr Gln		
1940	1945	1950
Val Leu Ser Ser Leu Thr Ile Thr Ser Leu Leu Arg Arg Leu His		
1955	1960	1965
Ala Trp Ile Thr Glu Asp Cys Pro Val Pro Cys Ser Gly Ser Trp		
1970	1975	1980
Leu Gln Asp Ile Trp Asp Trp Val Cys Ser Ile Leu Thr Asp Phe		
1985	1990	1995
Lys Asn Trp Leu Ser Ser Lys Leu Leu Pro Lys Met Pro Gly Ile		
2000	2005	2010
Pro Phe Ile Ser Cys Gln Lys Gly Tyr Lys Gly Val Trp Ala Gly		
2015	2020	2025
Thr Gly Val Met Thr Thr Arg Cys Pro Cys Gly Ala Asn Ile Ser		
2030	2035	2040
Gly His Val Arg Met Gly Thr Met Lys Ile Thr Gly Pro Lys Thr		
2045	2050	2055
Cys Leu Asn Leu Trp Gln Gly Thr Phe Pro Ile Asn Cys Tyr Thr		
2060	2065	2070
Glu Gly Pro Cys Val Pro Lys Pro Pro Pro Asn Tyr Lys Thr Ala		
2075	2080	2085
Ile Trp Arg Val Ala Ala Ser Glu Tyr Val Glu Val Thr Gln His		
2090	2095	2100
Gly Ser Phe Ser Tyr Val Thr Gly Leu Thr Ser Asp Asn Leu Lys		
2105	2110	2115
Val Pro Cys Gln Val Pro Ala Pro Glu Phe Phe Ser Trp Val Asp		

2120	2125	2130
Gly Val Gln Ile His Arg Phe Ala Pro Val Pro Gly Pro Phe Phe		
2135	2140	2145
Arg Asp Glu Val Thr Phe Thr Val Gly Leu Asn Ser Phe Val Val		
2150	2155	2160
Gly Ser Gln Leu Pro Cys Asp Pro Glu Pro Asp Thr Glu Val Leu		
2165	2170	2175
Ala Ser Met Leu Thr Asp Pro Ser His Ile Thr Ala Glu Ala Ala		
2180	2185	2190
Ala Arg Arg Leu Ala Arg Gly Ser Pro Pro Ser Gln Ala Ser Ser		
2195	2200	2205
Ser Ala Ser Gln Leu Ser Ala Pro Ser Leu Lys Ala Thr Cys Thr		
2210	2215	2220
Thr His Lys Thr Ala Tyr Asp Cys Asp Met Val Asp Ala Asn Leu		
2225	2230	2235
Phe Met Gly Gly Asp Val Thr Arg Ile Glu Ser Asp Ser Lys Val		
2240	2245	2250
Ile Val Leu Asp Ser Leu Asp Ser Met Thr Glu Val Glu Asp Asp		
2255	2260	2265
Arg Glu Pro Ser Val Pro Ser Glu Tyr Leu Ile Lys Arg Arg Lys		
2270	2275	2280
Phe Pro Pro Ala Leu Pro Pro Trp Ala Arg Pro Asp Tyr Asn Pro		
2285	2290	2295
Val Leu Ile Glu Thr Trp Lys Arg Pro Gly Tyr Glu Pro Pro Thr		
2300	2305	2310
Val Leu Gly Cys Ala Leu Pro Pro Thr Pro Gln Thr Pro Val Pro		
2315	2320	2325
Pro Pro Arg Arg Arg Arg Ala Lys Val Leu Thr Gln Asp Asn Val		
2330	2335	2340

Glu Gly Val Leu Arg Glu Met Ala Asp Lys Val Leu Ser Pro Leu			
2345	2350	2355	
Gln Asp Asn Asn Asp Ser Gly His Ser Thr Gly Ala Asp Thr Gly			
2360	2365	2370	
Gly Asp Ile Val Gln Gln Pro Ser Asp Glu Thr Ala Ala Ser Glu			
2375	2380	2385	
Ala Gly Ser Leu Ser Ser Met Pro Pro Leu Glu Gly Glu Pro Gly			
2390	2395	2400	
Asp Pro Asp Leu Glu Phe Glu Pro Val Gly Ser Ala Pro Pro Ser			
2405	2410	2415	
Glu Gly Glu Cys Glu Val Ile Asp Ser Asp Ser Lys Ser Trp Ser			
2420	2425	2430	
Thr Val Ser Asp Gln Glu Asp Ser Val Ile Cys Cys Ser Met Ser			
2435	2440	2445	
Tyr Ser Trp Thr Gly Ala Leu Ile Thr Pro Cys Gly Pro Glu Glu			
2450	2455	2460	
Glu Lys Leu Pro Ile Asn Pro Leu Ser Asn Ser Leu Met Arg Phe			
2465	2470	2475	
His Asn Lys Val Tyr Ser Thr Thr Ser Arg Ser Ala Ser Leu Arg			
2480	2485	2490	
Ala Lys Lys Val Thr Phe Asp Arg Val Gln Val Leu Asp Ala His			
2495	2500	2505	
Tyr Asp Ser Val Leu Gln Asp Val Lys Arg Ala Ala Ser Lys Val			
2510	2515	2520	
Ser Ala Arg Leu Leu Thr Val Glu Glu Ala Cys Ala Leu Thr Pro			
2525	2530	2535	
Pro His Ser Ala Lys Ser Arg Tyr Gly Phe Gly Ala Lys Glu Val			
2540	2545	2550	
Arg Ser Leu Ser Arg Arg Ala Val Asn His Ile Arg Ser Val Trp			

2555	2560	2565
Glu Asn Leu Leu Glu Asp Gln His Thr Pro Ile Asp Thr Thr Ile		
2570	2575	2580
Met Ala Lys Asn Glu Val Phe Cys Ile Asp Pro Thr Lys Gly Gly		
2585	2590	2595
Lys Lys Pro Ala Arg Leu Ile Val Tyr Pro Asp Leu Gly Val Arg		
2600	2605	2610
Val Cys Glu Lys Met Ala Leu Tyr Asp Ile Ala Gln Lys Leu Pro		
2615	2620	2625
Lys Ala Ile Met Gly Pro Ser Tyr Gly Phe Gln Tyr Ser Pro Ala		
2630	2635	2640
Glu Arg Val Asp Phe Leu Leu Lys Ala Trp Gly Ser Lys Lys Asp		
2645	2650	2655
Pro Met Gly Phe Ser Tyr Asp Thr Arg Cys Phe Asp Ser Thr Val		
2660	2665	2670
Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr Gln Ala Cys		
2675	2680	2685
Ser Leu Pro Gln Glu Ala Arg Thr Val Ile His Ser Leu Thr Glu		
2690	2695	2700
Arg Leu Tyr Val Gly Gly Pro Met Thr Asn Ser Lys Gly Gln Ser		
2705	2710	2715
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser		
2720	2725	2730
Met Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ala Cys		
2735	2740	2745
Lys Ala Ala Gly Ile Val Asp Pro Val Met Leu Val Cys Gly Asp		
2750	2755	2760
Asp Leu Val Val Ile Ser Glu Ser Gln Gly Asn Glu Glu Asp Glu		
2765	2770	2775

Arg Asn Leu Arg Ala Phe Thr Glu Ala Met Thr Arg Tyr Ser Ala			
	2780	2785	2790
Pro Pro Gly Asp Leu Pro Arg Pro Glu Tyr Asp Leu Glu Leu Ile			
	2795	2800	2805
Thr Ser Cys Ser Ser Asn Val Ser Val Ala Leu Asp Ser Arg Gly			
	2810	2815	2820
Arg Arg Arg Tyr Phe Leu Thr Arg Asp Pro Thr Thr Pro Ile Thr			
	2825	2830	2835
Arg Ala Ala Trp Glu Thr Val Arg His Ser Pro Val Asn Ser Trp			
	2840	2845	2850
Leu Gly Asn Ile Ile Gln Tyr Ala Pro Thr Ile Trp Val Arg Met			
	2855	2860	2865
Val Ile Met Thr His Phe Phe Ser Ile Leu Leu Ala Gln Asp Thr			
	2870	2875	2880
Leu Asn Gln Asn Leu Asn Phe Glu Met Tyr Gly Ala Val Tyr Ser			
	2885	2890	2895
Val Asn Pro Leu Asp Leu Pro Ala Ile Ile Glu Arg Leu His Gly			
	2900	2905	2910
Leu Glu Ala Phe Ser Leu His Thr Tyr Ser Pro His Glu Leu Ser			
	2915	2920	2925
Arg Val Ala Ala Thr Leu Arg Lys Leu Gly Ala Pro Pro Leu Arg			
	2930	2935	2940
Ala Trp Lys Ser Arg Ala Arg Ala Val Arg Ala Ser Leu Ile Ala			
	2945	2950	2955
Gln Gly Ala Arg Ala Ala Ile Cys Gly Arg Tyr Leu Phe Asn Trp			
	2960	2965	2970
Ala Val Lys Thr Lys Leu Lys Leu Thr Pro Leu Pro Glu Ala Ser			
	2975	2980	2985
Arg Leu Asp Leu Ser Gly Trp Phe Thr Val Gly Ala Gly Gly Gly			

	2990	2995	3000
Asp Ile Tyr His Ser Val Ser His Ala Arg Pro Arg Leu Leu Leu			
	3005	3010	3015
Leu Cys Leu Leu Leu Leu Ser Val Gly Val Gly Ile Phe Leu Leu			
	3020	3025	3030
Pro Ala Arg			
3033			

Sequence ID No. 9
 Sequence Length: 3,033
 Sequence Type: amino acid
 Topology: linear
 Molecule Type: protein

Met	Ser	Thr	Asn	Pro	Lys	Pro	Gln	Arg	Lys	Thr	Lys	Arg	Asn	Thr
				5					10					15
Asn	Arg	Arg	Pro	Gln	Asp	Val	Lys	Phe	Pro	Gly	Gly	Gly	Gln	Ile
				20					25					30
Val	Gly	Gly	Val	Tyr	Leu	Leu	Pro	Arg	Arg	Gly	Pro	Arg	Leu	Gly
				35					40					45
Val	Arg	Ala	Thr	Arg	Lys	Thr	Ser	Glu	Arg	Ser	Gln	Pro	Arg	Gly
				50					55					60
Arg	Arg	Gln	Pro	Ile	Pro	Lys	Asp	Arg	Arg	Ser	Thr	Gly	Lys	Ser
				65					70					75
Trp	Gly	Lys	Pro	Gly	Tyr	Pro	Trp	Pro	Leu	Tyr	Gly	Asn	Glu	Gly
				80					85					90
Cys	Gly	Trp	Ala	Gly	Trp	Leu	Leu	Ser	Pro	Arg	Gly	Ser	Arg	Pro
				95					100					105
Thr	Trp	Gly	Pro	Thr	Asp	Pro	Arg	His	Arg	Ser	Arg	Asn	Leu	Gly
				110					115					120
Arg	Val	Ile	Asp	Thr	Ile	Thr	Cys	Gly	Phe	Ala	Asp	Leu	Met	Gly
				125					130					135
Tyr	Ile	Pro	Val	Val	Gly	Ala	Pro	Val	Gly	Gly	Val	Ala	Arg	Ala
				140					145					150
Leu	Ala	His	Gly	Val	Arg	Val	Leu	Glu	Asp	Gly	Ile	Asn	Tyr	Ala
				155					160					165

Thr Gly Asn Leu Pro Gly Cys Ser Phe Ser Ile Phe Leu Leu Ala	170	175	180
Leu Leu Ser Cys Val Thr Met Pro Val Ser Ala Val Glu Val Arg	185	190	195
Asn Ile Ser Ser Ser Tyr Tyr Ala Thr Asn Asp Cys Ser Asn Asn	200	205	210
Ser Ile Thr Trp Gln Leu Thr Asp Ala Val Leu His Leu Pro Gly	215	220	225
Cys Val Pro Cys Glu Asn Asp Asn Gly Thr Leu Arg Cys Trp Ile	230	235	240
Gln Val Thr Pro Asp Val Ala Val Lys His Arg Gly Ala Leu Thr	245	250	255
Arg Ser Leu Arg Thr His Val Asp Met Ile Val Met Ala Ala Thr	260	265	270
Ala Cys Ser Ala Leu Tyr Val Gly Asp Val Cys Gly Ala Val Met	275	280	285
Ile Leu Ser Gln Ala Phe Met Val Ser Pro Gln Arg His Asn Phe	290	295	300
Thr Gln Glu Cys Asn Cys Ser Ile Tyr Gln Gly His Ile Thr Gly	305	310	315
His Arg Met Ala Trp Asp Met Met Leu Asn Trp Ser Pro Thr Leu	320	325	330
Ala Met Ile Leu Ala Tyr Ala Ala Arg Val Pro Glu Leu Val Leu	335	340	345
Glu Ile Ile Phe Gly Gly His Trp Gly Val Ala Phe Gly Leu Gly	350	355	360
Tyr Phe Ser Met Gln Gly Ala Trp Ala Lys Val Val Ala Ile Leu	365	370	375
Leu Leu Val Ala Gly Val Asp Ala Ser Thr Tyr Ser Thr Gly Gln			

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380	385	390
Gln Ala Gly Arg Ala Ala Tyr Gly Ile Ser Ser Leu Phe Asn Thr		
395	400	405
Gly Ala Lys Gln Asn Leu His Leu Ile Asn Thr Asn Gly Ser Trp		
410	415	420
His Ile Asn Arg Thr Ala Leu Asn Cys Asn Asp Ser Leu Glu Thr		
425	430	435
Gly Phe Ile Ala Ser Leu Val Tyr Tyr Arg Arg Phe Asn Ser Ser		
440	445	450
Gly Cys Pro Glu Arg Leu Ser Ser Cys Arg Gly Leu Asp Asp Phe		
455	460	465
Arg Ile Gly Trp Gly Thr Leu Glu Tyr Glu Thr Asn Val Thr Asn		
470	475	480
Asp Glu Asp Met Arg Pro Tyr Cys Trp His Tyr Pro Pro Arg Pro		
485	490	495
Cys Gly Ile Val Pro Ala Arg Thr Val Cys Gly Pro Val Tyr Cys		
500	505	510
Phe Thr Pro Ser Pro Val Val Val Gly Thr Thr Asp Lys Gln Gly		
515	520	525
Val Pro Thr Tyr Thr Trp Gly Glu Asn Glu Thr Asp Val Phe Leu		
530	535	540
Leu Asn Ser Thr Arg Pro Pro Arg Gly Ala Trp Phe Gly Cys Thr		
545	550	555
Trp Met Asn Gly Thr Gly Phe Thr Lys Thr Cys Gly Ala Pro Pro		
560	565	570
Cys Arg Ile Arg Lys Asp Tyr Asn Ser Thr Ile Asp Leu Leu Cys		
575	580	585
Pro Thr Asp Cys Phe Arg Lys His Pro Asp Ala Thr Tyr Leu Lys		
590	595	600

Cys Gly Ala Gly Pro Trp Leu Thr Pro Arg Cys Leu Val Asp Tyr		
	605	615
Pro Tyr Arg Leu Trp His Tyr Pro Cys Thr Val Asn Phe Thr Ile		
	620	630
Phe Lys Ala Arg Met Tyr Val Gly Gly Val Glu His Arg Phe Ser		
	635	645
Ala Ala Cys Asn Phe Thr Arg Gly Asp Arg Cys Arg Leu Glu Asp		
	650	660
Arg Asp Arg Gly Gln Gln Ser Pro Leu Leu His Ser Thr Thr Glu		
	665	675
Trp Ala Val Phe Pro Cys Ser Phe Ser Asp Leu Pro Ala Leu Ser		
	680	690
Thr Gly Leu Leu His Leu His Gln Asn Ile Val Asp Val Gln Tyr		
	695	705
Leu Tyr Gly Leu Ser Pro Ala Leu Thr Arg Tyr Ile Val Lys Trp		
	710	720
Glu Trp Val Ile Leu Leu Phe Leu Leu Leu Ala Asp Ala Arg Val		
	725	735
Cys Ala Cys Leu Trp Met Leu Asn Ile Leu Gly Gln Ala Glu Ala		
	740	750
Ala Leu Glu Lys Leu Ile Ile Leu His Ser Ala Ser Ala Ala Ser		
	755	765
Ala Asn Gly Pro Leu Trp Phe Phe Ile Phe Phe Thr Ala Ala Trp		
	770	780
Tyr Leu Lys Gly Arg Val Val Pro Val Ala Thr Tyr Ser Val Leu		
	785	795
Gly Leu Trp Ser Phe Leu Leu Leu Val Leu Ala Leu Pro Gln Gln		
	800	810
Ala Tyr Ala Leu Asp Ala Ala Glu Gln Gly Glu Leu Gly Leu Ala		

815	820	825
Ile Leu Val Ile Ile Ser Ile Phe Thr Leu Thr Pro Ala Tyr Lys		
830	835	840
Ile Leu Leu Ser Arg Ser Val Trp Trp Leu Ser Tyr Met Leu Val		
845	850	855
Leu Ala Glu Ala Gln Ile Gln Gln Trp Val Pro Pro Leu Glu Val		
860	865	870
Arg Gly Gly Arg Asp Gly Ile Ile Trp Val Ala Val Ile Leu His		
875	880	885
Pro Arg Leu Val Phe Glu Val Thr Lys Trp Leu Leu Ala Ile Leu		
890	895	900
Gly Pro Ala Tyr Leu Leu Arg Ala Ser Leu Leu Arg Ile Pro Tyr		
905	910	915
Phe Val Arg Ala His Ala Leu Leu Arg Val Cys Thr Leu Val Lys		
920	925	930
His Leu Ala Gly Ala Arg Tyr Ile Gln Met Leu Leu Ile Thr Ile		
935	940	945
Gly Arg Trp Thr Gly Thr Tyr Ile Tyr Asp His Leu Ser Pro Leu		
950	955	960
Ser Thr Trp Ala Ala Gln Gly Leu Arg Asp Leu Ala Ile Ala Val		
965	970	975
Glu Pro Val Val Phe Ser Pro Met Glu Lys Lys Val Ile Val Trp		
980	985	990
Gly Ala Glu Thr Val Ala Cys Gly Asp Ile Leu His Gly Leu Pro		
995	1000	1005
Val Ser Ala Arg Leu Gly Arg Glu Val Leu Leu Gly Pro Ala Asp		
1010	1015	1020
Gly Tyr Thr Ser Lys Gly Trp Asn Leu Leu Ala Pro Ile Thr Ala		
1025	1030	1035

Tyr Thr Gln Gln Thr Arg Gly Leu Leu Gly Ala Ile Val Val Ser			
	1040	1045	1050
Leu Thr Gly Arg Asp Lys Asn Glu Gln Ala Gly Gln Val Gln Val			
	1055	1060	1065
Leu Ser Ser Val Thr Gln Thr Phe Leu Gly Thr Ser Ile Ser Gly			
	1070	1075	1080
Val Leu Trp Thr Val Tyr His Gly Ala Gly Asn Lys Thr Leu Ala			
	1085	1090	1095
Gly Pro Lys Gly Pro Val Thr Gln Met Tyr Thr Ser Ala Glu Gly			
	1100	1105	1110
Asp Leu Val Gly Trp Pro Ser Pro Pro Gly Thr Lys Ser Leu Asp			
	1115	1120	1125
Pro Cys Thr Cys Gly Ala Val Asp Leu Tyr Leu Val Thr Arg Asn			
	1130	1135	1140
Ala Asp Val Ile Pro Val Arg Arg Lys Asp Asp Arg Arg Gly Ala			
	1145	1150	1155
Leu Leu Ser Pro Arg Pro Leu Ser Thr Leu Lys Gly Ser Ser Gly			
	1160	1165	1170
Gly Pro Val Leu Cys Ser Arg Gly His Ala Val Gly Leu Phe Arg			
	1175	1180	1185
Ala Ala Val Cys Ala Arg Gly Val Ala Lys Ser Ile Asp Phe Ile			
	1190	1195	1200
Pro Val Glu Ser Leu Asp Ile Ala Thr Arg Thr Pro Ser Phe Ser			
	1205	1210	1215
Asp Asn Ser Ala Pro Pro Ala Val Pro Gln Ser Tyr Gln Val Gly			
	1220	1225	1230
Tyr Leu His Ala Pro Thr Gly Ser Gly Lys Ser Thr Lys Val Pro			
	1235	1240	1245
Ala Ala Tyr Ala Ser Gln Gly Tyr Lys Val Leu Val Leu Asn Pro			

1250	1255	1260
Ser Val Ala Ala Thr Leu Gly Phe Gly Ala Tyr Met Ser Lys Ala		
1265	1270	1275
His Gly Ile Asn Pro Asn Ile Arg Thr Gly Val Arg Thr Val Thr		
1280	1285	1290
Thr Gly Asp Ser Ile Thr Tyr Ser Thr Tyr Gly Lys Phe Ile Ala		
1295	1300	1305
Asp Gly Gly Cys Ala Ala Gly Ala Tyr Asp Ile Ile Ile Cys Asp		
1310	1315	1320
Glu Cys His Ser Val Asp Ala Thr Thr Ile Leu Gly Ile Gly Thr		
1325	1330	1335
Val Leu Asp Gln Ala Glu Thr Ala Gly Val Arg Leu Val Val Leu		
1340	1345	1350
Ala Thr Ala Thr Pro Pro Gly Thr Val Thr Thr Pro His Ser Asn		
1355	1360	1365
Ile Glu Glu Val Ala Leu Gly His Glu Gly Glu Ile Pro Phe Tyr		
1370	1375	1380
Gly Lys Ala Ile Pro Leu Ala Phe Ile Lys Gly Gly Arg His Leu		
1385	1390	1395
Ile Phe Cys His Ser Lys Lys Lys Cys Asp Glu Leu Ala Ala Ala		
1400	1405	1410
Leu Arg Gly Thr Gly Val Asn Ala Val Ala Tyr Tyr Arg Gly Leu		
1415	1420	1425
Asp Val Ser Val Ile Pro Thr Gln Gly Asp Val Val Val Val Ala		
1430	1435	1440
Thr Asp Ala Leu Met Thr Gly Tyr Thr Gly Asp Phe Asp Ser Val		
1445	1450	1455
Ile Asp Cys Asn Val Ala Val Ser Gln Ile Val Asp Phe Ser Leu		
1460	1465	1470

Asp Pro Thr Phe Thr Ile Thr Thr Gln Thr Val Pro Gln Asp Ala	1475	1480	1485
Val Ser Arg Ser Gln Arg Arg Gly Arg Thr Gly Arg Gly Arg Leu	1490	1495	1500
Gly Ile Tyr Arg Tyr Val Ser Ser Gly Glu Gly Pro Ser Gly Met	1505	1510	1515
Phe Asp Ser Val Val Pro Cys Glu Cys Tyr Asp Ala Gly Ala Ala	1520	1525	1530
Trp Tyr Glu Leu Thr Pro Ala Glu Thr Thr Val Arg Leu Arg Ala	1535	1540	1545
Tyr Phe Asn Thr Pro Gly Leu Pro Val Cys Gln Asp His Leu Glu	1550	1555	1560
Phe Trp Glu Ala Val Phe Thr Gly Leu Thr His Ile Asn Ala His	1565	1570	1575
Phe Leu Ser Gln Thr Lys Gln Gly Gly Glu Asn Phe Ala Tyr Leu	1580	1585	1590
Thr Ala Tyr Gln Ala Thr Val Cys Ala Arg Ala Lys Ala Pro Pro	1595	1600	1605
Pro Ser Trp Asp Val Met Trp Lys Cys Leu Thr Arg Leu Lys Pro	1610	1615	1620
Thr Leu Thr Gly Pro Thr Pro Leu Leu Tyr Arg Leu Gly Ala Val	1625	1630	1635
Thr Asn Glu Val Thr Leu Thr His Pro Val Thr Lys Tyr Ile Ala	1640	1645	1650
Thr Cys Met Gln Ala Asp Leu Glu Ile Met Thr Ser Ser Trp Val	1655	1660	1665
Leu Ala Gly Gly Val Leu Ala Ala Val Ala Ala Tyr Cys Leu Ala	1670	1675	1680
Thr Gly Cys Ile Ser Ile Ile Gly Arg Leu His Leu Asn Asp Arg			

1685	1690	1695
Val Val Val Thr Pro Asp Lys Glu Ile Leu Tyr Glu Ala Phe Asp		
1700	1705	1710
Glu Met Glu Glu Cys Ala Ser Lys Ala Ala Leu Ile Glu Glu Gly		
1715	1720	1725
Gln Arg Met Ala Glu Met Leu Lys Ser Lys Ile Gln Gly Leu Leu		
1730	1735	1740
Gln Gln Ala Thr Arg Gln Ala Gln Gly Met Gln Pro Ala Ile Gln		
1745	1750	1755
Ser Ser Trp Pro Lys Leu Glu Gln Phe Trp Ala Lys His Met Trp		
1760	1765	1770
Asn Phe Ile Ser Gly Ile Gln Tyr Leu Ala Gly Leu Ser Thr Leu		
1775	1780	1785
Pro Gly Asn Pro Ala Val Ala Ser Met Met Ala Phe Ser Ala Ala		
1790	1795	1800
Leu Thr Ser Pro Leu Pro Thr Ser Thr Thr Ile Leu Leu Asn Ile		
1805	1810	1815
Met Gly Gly Trp Leu Ala Ser Gln Ile Ala Pro Pro Ala Gly Ala		
1820	1825	1830
Thr Gly Phe Val Val Ser Gly Leu Val Gly Ala Ala Val Gly Ser		
1835	1840	1845
Ile Gly Leu Gly Lys Ile Leu Val Asp Val Leu Ala Gly Tyr Gly		
1850	1855	1860
Ala Gly Ile Ser Gly Ala Leu Val Ala Phe Lys Ile Met Ser Gly		
1865	1870	1875
Glu Lys Pro Thr Val Glu Asp Val Val Asn Leu Leu Pro Ala Ile		
1880	1885	1890
Leu Ser Pro Gly Ala Leu Val Val Gly Val Ile Cys Ala Ala Ile		
1895	1900	1905

Leu Arg Arg His Val Gly Gln Gly Glu Gly Ala Val Gln Trp Met		
1910	1915	1920
Asn Arg Leu Ile Ala Phe Ala Ser Arg Gly Asn His Val Ala Pro		
1925	1930	1935
Thr His Tyr Val Val Glu Ser Asp Ala Ser Gln Arg Val Thr Gln		
1940	1945	1950
Val Leu Ser Ser Leu Thr Ile Thr Ser Leu Leu Arg Arg Leu His		
1955	1960	1965
Ala Trp Ile Thr Glu Asp Cys Pro Ile Pro Cys Ser Gly Ser Trp		
1970	1975	1980
Leu Gln Asp Ile Trp Asp Trp Val Cys Ser Ile Leu Thr Asp Phe		
1985	1990	1995
Lys Asn Trp Leu Ser Ser Lys Leu Leu Pro Lys Met Pro Gly Ile		
2000	2005	2010
Pro Phe Ile Ser Cys Gln Lys Gly Tyr Lys Gly Val Trp Ala Gly		
2015	2020	2025
Thr Gly Val Met Thr Thr Arg Tyr Pro Cys Gly Ala Asn Ile Ser		
2030	2035	2040
Gly His Val Arg Met Gly Thr Met Lys Ile Thr Gly Pro Lys Thr		
2045	2050	2055
Cys Leu Asn Leu Trp Gln Gly Thr Phe Pro Ile Asn Cys Tyr Thr		
2060	2065	2070
Glu Gly Pro Cys Val Pro Lys Pro Pro Pro Asn Tyr Lys Thr Ala		
2075	2080	2085
Ile Trp Arg Val Ala Ala Ser Glu Tyr Val Glu Val Thr Gln His		
2090	2095	2100
Gly Ser Phe Ser Tyr Val Thr Gly Leu Thr Ser Asp Asn Leu Lys		
2105	2110	2115
Val Pro Cys Gln Val Pro Ala Pro Glu Phe Phe Ser Trp Val Asp		

2120	2125	2130
Gly Val Gln Ile His Arg Phe Ala Pro Val Pro Gly Pro Phe Phe		
2135	2140	2145
Arg Asp Glu Val Thr Phe Thr Val Gly Leu Asn Ser Phe Val Val		
2150	2155	2160
Gly Ser Gln Leu Pro Cys Asp Pro Glu Pro Asp Thr Glu Val Leu		
2165	2170	2175
Ala Ser Met Leu Thr Asp Pro Ser His Ile Thr Ala Glu Ala Ala		
2180	2185	2190
Ala Arg Arg Leu Ala Arg Gly Ser Pro Pro Ser Gln Ala Ser Ser		
2195	2200	2205
Ser Ala Ser Gln Leu Ser Ala Pro Ser Leu Lys Ala Thr Cys Thr		
2210	2215	2220
Thr His Lys Thr Ala Tyr Asp Cys Asp Met Val Asp Ala Asn Leu		
2225	2230	2235
Phe Met Gly Gly Asp Val Thr Arg Ile Glu Ser Asp Ser Lys Val		
2240	2245	2250
Ile Val Leu Asp Ser Leu Asp Ser Met Thr Glu Val Glu Asp Asp		
2255	2260	2265
Arg Glu Pro Ser Val Pro Ser Glu Tyr Leu Ile Lys Arg Arg Lys		
2270	2275	2280
Phe Pro Pro Ala Leu Pro Pro Trp Ala Arg Pro Asp Tyr Asn Pro		
2285	2290	2295
Val Leu Ile Glu Thr Trp Lys Arg Pro Gly Tyr Glu Pro Pro Thr		
2300	2305	2310
Val Leu Gly Cys Ala Leu Pro Pro Thr Leu Gln Thr Pro Val Pro		
2315	2320	2325
Pro Pro Arg Arg Arg Arg Ala Lys Ile Leu Thr Gln Asp Asp Val		
2330	2335	2340

Glu Gly Ile Leu Arg Glu Met Ala Asp Lys Val Leu Ser Pro Leu		
2345	2350	2355
Gln Asp Asn Asn Asp Ser Gly His Ser Thr Gly Ala Asp Thr Gly		
2360	2365	2370
Gly Asp Ile Val Gln Gln Pro Ser Asp Glu Thr Ala Ala Ser Glu		
2375	2380	2385
Ala Gly Ser Leu Ser Ser Met Pro Pro Leu Glu Gly Glu Pro Gly		
2390	2395	2400
Asp Pro Asp Leu Glu Phe Glu Pro Val Gly Ser Ala Pro Pro Ser		
2405	2410	2415
Glu Gly Glu Cys Glu Val Ile Asp Ser Asp Ser Lys Ser Trp Ser		
2420	2425	2430
Thr Val Ser Asp Gln Glu Asp Ser Val Ile Cys Cys Ser Met Ser		
2435	2440	2445
Tyr Ser Trp Thr Gly Ala Leu Ile Thr Pro Cys Gly Pro Glu Glu		
2450	2455	2460
Glu Lys Leu Pro Ile Asn Pro Leu Ser Asn Ser Leu Met Arg Phe		
2465	2470	2475
His Asn Lys Val Tyr Ser Thr Thr Ser Arg Ser Ala Ser Leu Arg		
2480	2485	2490
Ala Lys Lys Val Thr Phe Asp Arg Val Gln Val Leu Asp Ala His		
2495	2500	2505
Tyr Asp Ser Val Leu Gln Asp Val Lys Arg Ala Ala Ser Lys Val		
2510	2515	2520
Gly Ala Arg Leu Leu Thr Val Glu Glu Ala Cys Ala Leu Thr Pro		
2525	2530	2535
Pro His Ser Ala Lys Ser Arg Tyr Gly Phe Gly Ala Lys Glu Val		
2540	2545	2550
Arg Ser Leu Ser Arg Arg Ala Val Asn His Ile Arg Ser Val Trp		

2555	2560	2565
Glu Asn Leu Leu Glu Asp Gln Arg Thr Pro Ile Asp Thr Thr Ile		
2570	2575	2580
Met Ala Lys Asn Glu Val Phe Cys Ile Asp Pro Thr Lys Gly Gly		
2585	2590	2595
Lys Lys Pro Ala Arg Leu Ile Val Tyr Pro Asp Leu Gly Val Arg		
2600	2605	2610
Val Cys Glu Lys Met Ala Leu Tyr Asp Ile Thr Gln Lys Leu Pro		
2615	2620	2625
Lys Ala Ile Met Gly Pro Ser Tyr Gly Phe Gln Tyr Ser Pro Ala		
2630	2635	2640
Glu Arg Val Asp Phe Leu Leu Lys Ala Trp Gly Ser Lys Lys Asp		
2645	2650	2655
Pro Met Gly Phe Ser Tyr Asp Thr Arg Cys Phe Asp Ser Thr Val		
2660	2665	2670
Thr Glu Arg Asp Ile Arg Thr Glu Glu Ser Ile Tyr Gln Ala Cys		
2675	2680	2685
Ser Leu Pro Gln Glu Ala Arg Thr Val Ile His Ser Leu Thr Glu		
2690	2695	2700
Arg Leu Tyr Val Gly Gly Pro Met Thr Asn Ser Lys Gly Gln Ser		
2705	2710	2715
Cys Gly Tyr Arg Arg Cys Arg Ala Ser Gly Val Phe Thr Thr Ser		
2720	2725	2730
Met Gly Asn Thr Met Thr Cys Tyr Ile Lys Ala Leu Ala Ala Cys		
2735	2740	2745
Lys Ala Ala Gly Ile Val Asp Pro Val Met Leu Val Cys Gly Asp		
2750	2755	2760
Asp Leu Val Val Ile Ser Glu Ser Gln Gly Asn Glu Glu Asp Glu		
2765	2770	2775

Arg Asn Leu Arg Ala Phe Thr Glu Ala Met Thr Arg Tyr Ser Ala			
	2780	2785	2790
Pro Pro Gly Asp Leu Pro Arg Pro Glu Tyr Asp Leu Glu Leu Ile			
	2795	2800	2805
Thr Ser Cys Ser Ser Asn Val Ser Val Ala Leu Asp Ser Arg Gly			
	2810	2815	2820
Arg Arg Arg Tyr Phe Leu Thr Arg Asp Pro Thr Thr Pro Ile Thr			
	2825	2830	2835
Arg Ala Ala Trp Glu Thr Val Arg His Ser Pro Val Asn Ser Trp			
	2840	2845	2850
Leu Gly Asn Ile Ile Gln Tyr Ala Pro Thr Ile Trp Val Arg Met			
	2855	2860	2865
Val Ile Met Thr His Phe Phe Ser Ile Leu Leu Ala Gln Asp Thr			
	2870	2875	2880
Leu Asn Gln Asn Leu Asn Phe Glu Met Tyr Gly Ala Val Tyr Ser			
	2885	2890	2895
Val Asn Pro Leu Asp Leu Pro Ala Ile Ile Glu Arg Leu His Gly			
	2900	2905	2910
Leu Glu Ala Phe Ser Leu His Thr Tyr Ser Pro His Glu Leu Ser			
	2915	2920	2925
Arg Val Ala Ala Thr Leu Arg Lys Leu Gly Ala Pro Pro Leu Arg			
	2930	2935	2940
Ala Trp Lys Ser Arg Ala Arg Ala Val Arg Ala Ser Leu Ile Ala			
	2945	2950	2955
Gln Gly Ala Arg Ala Ala Ile Cys Gly Arg Tyr Leu Phe Asn Trp			
	2960	2965	2970
Ala Val Lys Thr Lys Leu Lys Leu Thr Pro Leu Pro Glu Ala Ser			
	2975	2980	2985
Arg Leu Asp Leu Ser Gly Trp Phe Thr Val Gly Ala Gly Gly Gly			